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(54) Title: VARIANTS OF ALTERNATIVE SPLICING

(57) Abstract: The present invention concerns novel variants, amino acid and nucleic acid sequences obtained by alternative splicing of known sequences, expression vectors and host cells containing the variants' nucleic acid sequence, and antibodies reactive with the variants' products. The invention also concerns pharmaceutical compositions containing any of the above as well as methods of detection. A preferred example is the angiotensin converting enzyme (ACE) variant.

VARIANTS OF ALTERNATIVE SPLICING

FIELD OF THE INVENTION

The present invention concerns novel nucleic acid sequences, vectors and host cells containing them, amino acid sequences encoded by said sequences, and antibodies reactive with said amino acid sequences, as well as pharmaceutical
5 compositions comprising any of the above. The present invention further concerns methods for screening for candidate activators or deactivators utilizing said amino acid sequences.

BACKGROUND OF THE INVENTION

Alternative splicing (AS) is an important regulatory mechanism in higher
10 eukaryotes (P.A. Sharp, *Cell* 77, 805-8152 (1994). It is thought to be one of the most important mechanisms for differential expression related to tissue or development stage specificity. It is known to play a major role in numerous biological systems, including human antibody responses, and sex determination in *Drosophila*, (S. Stamm, M.Q. Zhang, T.G. Marr and D.M. Helfman, *Nucleic
15 Acids Research* 22, 1515-1526 (1994); B. Chabot, *Trends Genet.* 12, 472-478 (1996); R.E. Breitbart, A. Andreadis, B. Nadal-Ginard, *Annual Rev. Biochem.*, 56, 467-495 (1987); C.W. Smith, J.G. Patton, B. Nadal-Ginard, *Annu. Rev. Genet.*, 27, 527-577 (1989)).

Until recently it was commonly believed that alternative splicing existed in
20 only a small fraction of genes (about 5%). A recent observation based on literature survey of known genes revises this conservative estimate to as high as an estimate that at least 30% of human genes are alternatively spliced (M.S. Gelfand, I. Dubchak, I. Draluk and M. Zorn, *Nucleic Acids Research* 27, 301-302 (1999). The importance of the actual frequency of this phenomenon lies not only

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in the direct impact on the number of proteins created (100,000 human genes, for example, would be translated to a much higher number of proteins), but also in the diversity of functionality derived from the process.

Several mechanisms at different stages may be held responsible for the complexity of higher eukaryote which include: alternative splicing at the transcription level, RNA editing at the post-transcriptional level, and post-translational modifications are the ones characterized to date.

Angiotensin I-converting enzyme (ACE) is a peptidyl dipeptide hydrolase that is located mainly on the luminal surface of vascular endothelial cells but also in cells derived from the monocyte-macrophage system. Physiologically, ACE is a key enzyme in the renin-angiotensin system, converting angiotensin I into the potent vasopressor angiotensin II and also inactivating the vasodilator bradykinin.

Increased serum ACE activity (SACE) has been reported in pathologies involving stimulation of the monocytic cell line, primarily granulomatous diseases. Sarcoidosis is the most frequent and the better studied of these diseases; high SACE is not only a well-established marker for the diagnosis but is also a useful tool for following its course and evaluating the effect of therapy of this disease.

SACE can also be increased in nonsarcoidotic pulmonary granulomatous diseases such as silicosis and asbestosis, in extrathoracic granulomatous pathologies such as Gauchers disease and leprosis, and, to a lesser extent, in nongranulomatous disorders such as hyperthyroidism or cholestasis.

Decreased SACE has been reported in vascular pathologies involving an endothelial abnormality, such as deep vein thrombosis, and in endothelium dysfunctions related to the toxicity of chemo- and radiotherapy used in cancers, leukemias, and hematopoietic or organ transplantations.

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SACE is also of interest for monitoring arterial hypertension treated with specific synthetic ACE inhibitors.

Various methods have been developed for determining SACE activities. The most widely used is the spectrophotometric assay using hippuryl-histidyl-leucine as substrate. Fluorimetric and radiochemical assays using both classic and novel substrates have been proposed, but they are time consuming, require special apparatus, and are not suited to automation. Kinetic spectrophotometry of furylacryloyl-phenylalanyl-glycyl-glycine hydrolysis is now used extensively because it is easy to automatize.

Information obtained in the last decade indicates that angiotensin II increases the production of several autocrine factors, including transforming growth factor beta1 (TGF-beta1), tumor necrosis factor-alpha (TNF-alpha), and platelet-derived growth factor A chain (PDGF). Angiotensin also increases the release of other growth factors such as endothelin, platelet-activating factor (PAF), and interleukin 6. In addition, it increases the "activity" of nuclear factor-kappaB (NF-kappaB) and the synthesis of angiotensinogen. The emerging picture indicates that the actions of angiotensin II may be related to factors that are released or upregulated by angiotensin II, possibly through NF-kappaB.

20 GLOSSARY

In the following description and claims use will be made, at times, with a variety of terms, and the meaning of such terms as they should be construed in accordance with the invention is as follows:

25 *"Variant nucleic acid sequence"* – the sequence shown in any one of SEQ ID NO: 1 to SEQ ID NO: 87, native and known genes. It should be emphasized that the novel variants of the present invention are naturally occurring sequences resulting from alternative splicing of genes and not merely truncated, mutated or fragmented forms of known sequences which are artificially produced.

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"*Angiotensin converting enzyme variant (ACEV)*" - a sequence shown in SEQ ID NO: 57 or 85 sequences having at least 90% identity (see below) to said sequence and *fragments* (see below) of the above sequences of least 20 b.p. long. These sequences are sequences coding for a novel, naturally occurring, alternative splice variants of the mouse angiotensin converting enzyme which convert angiotensin I to angiotensin II by release of the terminal His-Lew resulting in increase of vasoconstrictor activity of angiotensin.

"*Variant product - also referred at times as the "variant protein" or "variant polypeptide"*" - is an amino acid sequence encoded by the variant nucleic acid sequence SEQ ID NO: 88 to SEQ ID NO: 174.

"*ACEV product or ACEV protein*" - amino acid coded by the ACEV nucleic acid which is a naturally occurring mRNA sequence obtained as a result of alternative splicing of the ACE gene. The amino acid sequence may be a peptide, a protein, as well as peptides or proteins having *chemically modified* amino acids (see below) such as a glycopeptide or glycoprotein. The variant products are shown in SEQ ID NO: 144 or 172. The term also includes *homologies* (see below) of said sequences in which one or more amino acids has been added, deleted, *substituted* (see below) or *chemically modified* (see below) as well as *fragments* (see below) of this sequence having at least 10 amino acids. The above two products may be secreted.

"*Nucleic acid sequence*" - a sequence composed of DNA nucleotides, RNA nucleotides or a combination of both types and may include natural nucleotides, chemically modified nucleotides and synthetic nucleotides.

"*Amino acid sequence*" - a sequence composed of any one of the 20 naturally appearing amino acids, amino acids which have been *chemically modified* (see below), or composed of synthetic amino acids.

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"Fragment of variant nucleic acid sequence" and **"fragment of ACEV nucleic acid sequence"** – novel short stretch of nucleic acid sequences of at least 20 b.p., which does not appear as a continuous stretch in the *original nucleic acid sequence* (see below). The fragment may be a sequence which was previously
5 undescribed in the context of the published RNA and which affects the amino acid sequence encoded by the known gene. For example, where the variant nucleic includes a sequence which was not included in the original sequence (for example a sequence which was an intron in the original sequence) the fragment may contain said additional sequence. The fragment may also be a region which
10 is not an intron, which was not present in the original sequence. For example where the variant lacks a non-terminal region which was present in the original sequence. The two stretches of nucleotides spanning this region (upstream and downstream) are brought together by splicing in the variant, but are spaced from each by the spliced out region in the original sequence and are thus not
15 continuous in the original sequence. A continuous stretch of nucleic acids comprising said two splicing stretches of nucleotides is not present in the original sequence and thus falls under the definition of fragment.

"Fragments of variant products" - novel amino acid sequences coded by the
20 **"fragment of variant nucleic acid sequence"** or **"fragment of ACEV nucleic acid sequence"** defined above.

"Homologues of variants" – amino acid sequences of variants in which one or more amino acids has been added, deleted or replaced. The addition, deletion or
25 replacement should be in the regions or adjacent to regions where the variant differs from the *original sequence* (see below).

"Conservative substitution" - refers to the substitution of an amino acid in one class by an amino acid of the same class, where a class is defined by common
30 physicochemical amino acid side chain properties and high substitution

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frequencies in homologous proteins found in nature, as determined, for example, by a standard Dayhoff frequency exchange matrix or BLOSUM matrix. [Six general classes of amino acid side chains have been categorized and include: Class I (Cys); Class II (Ser, Thr, Pro, Ala, Gly); Class III (Asn, Asp, Gln, Glu);
5 Class IV (His, Arg, Lys); Class V (Ile, Leu, Val, Met); and Class VI (Phe, Tyr, Trp). For example, substitution of an Asp for another class III residue such as Asn, Gln, or Glu, is a conservative substitution.

"Non-conservative substitution" - refers to the substitution of an amino acid in
10 one class with an amino acid from another class; for example, substitution of an Ala, a class II residue, with a class III residue such as Asp, Asn, Glu, or Gln.

"Chemically modified" - when referring to the product of the invention, means a product (protein) where at least one of its amino acid residues is modified either by
15 natural processes, such as processing or other post-translational modifications, or by chemical modification techniques which are well known in the art. Among the numerous known modifications typical, but not exclusive examples include: acetylation, acylation, amidation, ADP-ribosylation, glycosylation, GPI anchor formation, covalent attachment of a lipid or lipid derivative, methylation,
20 myristylation, pegylation, prenylation, phosphorylation, ubiquitination, or any similar process.

"Biologically active" - refers to the variant product having some sort of biological activity, for example, some physiologically measurable effect on target
25 cells, molecules or tissues.

"Immunologically active" defines the capability of a natural, recombinant or synthetic variant product, or any fragment thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.
30 Thus, for example, an immunologically active fragment of variant product

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denotes a fragment which retains some or all of the immunological properties of the variant product, e.g. can bind specific anti-variant product antibodies or which can elicit an immune response which will generate such antibodies or cause proliferation of specific immune cells which produce variant.

5

"Optimal alignment" - is defined as an alignment giving the highest percent identity score. Such alignment can be performed using a variety of commercially available sequence analysis programs, such as the local alignment program LALIGN using a ktup of 1, default parameters and the default PAM. A preferred
10 alignment is the one performed using the CLUSTAL-W program from MacVector (TM), operated with an open gap penalty of 10.0, an extended gap penalty of 0.1, and a BLOSUM similarity matrix. If a gap needs to be inserted into a first sequence to optimally align it with a second sequence, the percent identity is calculated using only the residues that are paired with a corresponding
15 amino acid residue (i.e., the calculation does not consider residues in the second sequences that are in the "gap" of the first sequence). In case of alignments of known gene sequences with that of the new variant, the optimal alignment invariably included aligning the identical parts of both sequences together, then keeping apart and unaligned the sections of the sequences that differ one from the
20 other.

"Having at least 90% identity" - with respect to two amino acid or nucleic acid sequence sequences, refers to the percentage of residues that are identical in the two sequences when the sequences are optimally aligned. Thus, 90% amino acid
25 sequence identity means that 90% of the amino acids in two or more optimally aligned polypeptide sequences are identical, however this definition explicitly excludes sequences which are 100% identical with the original sequence from which the variant of the invention was varied.

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"Isolated nucleic acid molecule having an variant nucleic acid sequence" - is a nucleic acid molecule that includes the coding variant nucleic acid sequence. Said isolated nucleic acid molecule may include the variant nucleic acid sequence as an independent insert; may include the variant nucleic acid sequence fused to an additional coding sequences, encoding together a fusion protein in which the variant coding sequence is the dominant coding sequence (for example, the additional coding sequence may code for a signal peptide); the variant nucleic acid sequence may be in combination with non-coding sequences, e.g., introns or control elements, such as promoter and terminator elements or 5' and/or 3' untranslated regions, effective for expression of the coding sequence in a suitable host; or may be a vector in which the variant protein coding sequence is a heterologous.

"Expression vector" - refers to vectors that have the ability to incorporate and express heterologous DNA fragments in a foreign cell. Many prokaryotic and eukaryotic expression vectors are known and/or commercially available. Selection of appropriate expression vectors is within the knowledge of those having skill in the art.

"Deletion" - is a change in either nucleotide or amino acid sequence in which one or more nucleotides or amino acid residues, respectively, are absent.

"Insertion" or "addition" - is that change in a nucleotide or amino acid sequence which has resulted in the addition of one or more nucleotides or amino acid residues, respectively, as compared to the naturally occurring sequence.

"Substitution" - replacement of one or more nucleotides or amino acids by different nucleotides or amino acids, respectively. As regards amino acid sequences the substitution may be conservative or non- conservative.

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"Antibody" – refers to IgG, IgM, IgD, IgA, or IgG antibody. The definition includes polyclonal antibodies or monoclonal antibodies. This term refers to whole antibodies or fragments of the antibodies comprising the antigen-binding domain of the anti-variant product antibodies, e.g. antibodies without the Fc portion, single chain antibodies, fragments consisting of essentially only the variable, antigen-binding domain of the antibody, etc.

Distinguishing antibody – an antibody capable of binding to the variant product and not the original amino acid sequence from which it has been varied, or an antibody capable of binding to the original nucleic acid sequence and not to the variant production.

"Activator" - as used herein, refers to a molecule which mimics the effect of the natural variant product or at times even increases or prolongs the duration of the biological activity of said product, as compared to that induced by the natural product. The mechanism may be by any mechanism known to prolonging activities of biological molecules such as binding to receptors; prolonging the lifetime of the molecules; increasing the activity of the molecules on its target; increasing the affinity of molecules to its receptor; inhibiting degradation or proteolysis of the molecules, or mimicking the biological activity of the variants on their targets, etc. Activators may be polypeptides, nucleic acids, carbohydrates, lipids, or derivatives thereof, or any other molecules which can bind to and activate the variant product.

"Deactivator" or ("Inhibitor") - refers to a molecule which modulates the activity of the variant product in an opposite manner to that of the activator, by decreasing or shortening the duration of the biological activity of the variant product. This may be done by any mechanism known to deactivate or inhibit biological molecules such as block of the receptor, block of active site, competition on binding site in target, enhancement of degradation, etc.

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Deactivators may be polypeptides, nucleic acids, carbohydrates, lipids, or derivatives thereof, or any other molecules which bind to and modulate the activity of said product.

- 5 **"Treating a disease"** - refers to administering a therapeutic substance effective to ameliorate symptoms associated with a disease, to lessen the severity or cure the disease, or to prevent the disease from occurring.

"Detection" - refers to a method of detection of a disease, disorder, pathological
10 or normal condition. This term may refer to detection of a predisposition to a disease as well as for establishing the prognosis of the patient by determining the severity of the disease.

"Probe" - the variant nucleic acid sequence, or a sequence complementary
15 therewith, when used to detect presence of other similar sequences in a sample. The detection is carried out by identification of hybridization complexes between the probe and the assayed sequence. The probe may be attached to a solid support or to a detectable label.

- 20 **"Original sequence"** - the amino acid or nucleic acid sequence from which the variant of the invention have been varied as a result of alternative slicing.

SUMMARY OF THE INVENTION

 The present invention is based on the finding of several novel, naturally occurring splice variants, which are naturally occurring sequences obtained by
25 alternative splicing of known genes. The novel splice variants of the invention are not merely truncated forms, fragments or mutations of known genes, but rather novel sequences which naturally occur within the body of individuals.

 In particular the present invention concerns variants of alternative splice variants of angiotensin converting enzyme (ACEV).

The term "*alternative splicing*" in the context of the present invention and claims refers to: intron inclusion, exon exclusion, addition or deletion of terminal sequences in the variant as compared to the original sequences, as well as to the possibility of "*intron retention*". Intron retention is an intermediate stage in the
5 processing of RNA transcripts, where prior to production of fully processed mRNA the intron (naturally spliced in the original sequence) is retained in the variant. These intermediately processed RNAs may have physiological significance and are also within the scope of the invention.

The novel variant products of the invention, including the ACEV-variant
10 (ACEV), may have the same physiological activity as the original peptide from which they have been varied (although perhaps at a different level); may have an opposite physiological activity from the activity featured by the original peptide from which they are varied; may have a completely different, unrelated activity to the activity of the original from which they are varied; or alternatively may have no
15 activity at all and this may lead to various diseases or pathological conditions. The novel variants of the invention may differ from the original sequence, from which they were varied by alternative splicing, by physiological properties not relating directly to their activities such as: tissue localization, temporal pattern of expression, rate of clearance, rate of degradation, manner of up- or down
20 regulation, association with co-factors and cellular elements etc.

The novel variants may also serve for detection purposes, i.e. their presence or level may be indicative of a disease, disorder, pathological or normal condition or alternatively the ratio between the level variants and the level original peptide from which they were varied, or the ratio to other variants may be indicative to a
25 disease, disorder, pathological or normal condition.

For example, for detectional purposes, it is possible to establish differential expression of various variants in various tissues. A certain variant may be expressed mainly in one tissue, while the original sequence from which it has been varied, or another variant may, be expressed mainly in another tissue.
30 Understanding of the distribution of the variants in various tissues may be helpful

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in basic research, for understanding the physiological function of the genes as well as may help in targeting pharmaceuticals or developing pharmaceuticals.

The study of the variants may also be helpful to distinguish various stages in the life cycles of the same type of cells which may also be helpful for development of pharmaceuticals for various pathological conditions in which cell cycles is non-normal, notably cancer.

Detection of various diseases in accordance with the invention is especially useful for detection of diseases which are associated with the function, (over function, under function, or malfunction) of proteins of the original sequence from which each variant of the invention has been obtained by alternative splicing. A list of the original proteins are given in the "Detailed Description" part of the specification. Thus, for example, if variant of SEQ ID NO: 3 is obtained from an original sequence which is coagulation factor XII, this sequence may be used to detect diseases involving excessive or diminished blood coagulation.

Thus the detection may by determination of the presence or the level of expression of the variant within a specific cell population, comprising said presence or level between various cell types in a tissue, between different tissues and between individuals.

Where the variant in the angiotensin converting enzyme (ACEV) the detection may be used for detection (including disposition) of one of the following diseases.

Cardiovascular diseases:

Including hypertension, neurological damage due to cerebral circulatory disorders, peripheral vascular diseases, arteriosclerosis, heart and kidney diseases relating to blood pressure, erection problems and migraine problems relating to circulation functions, heart failures (including recurrent infraction in patients with left ventricular dysfunction), acute phase of myocardial infarction, coronary arterial thrombosis and cardial insufficiency.

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Renal diseases:

Hypertension adrenal injury (particularly in patients with type I or II diabetes), diabetic neuropathy, renal function deterioration in glomerular diseases

Muscular diseases:

5 Diseases involving growth of smooth muscle cells such as hypertrophy.

Immune disorders:

Various autoimmune diseases and diseases involving inflammatory mechanisms, for example, autoimmune manifestation affects in sarcoidosis, generation of immune complex nephritis, autoimmune encephatomyelitis, marker
10 for chronic fatigue-immune dysfunction syndrome.

Multiple sclerosis:Cancer:

Especially those cancers effected by different growth factors including endothelia, platelet-activating factor (PAF) and interleukin 6. Examples of such
15 cancers are tumors of the vascular system, and leukemias.

Diabetes:

Sarcoidosis – a disease of unknown origin characterized by the formation of granulomatous lesions that appear especially in the liver, lungs, skin and lymph nodes.

20 Nonaroidotic Pulmonary Granulomatous Diseases:

Such as silicosis and asbestosis, in extrathoracic granulomatous pathologies such as Gauchers disease and leprosis, and, to a lesser extent, in nongranulomatous disorders such as hyperthyroidism or cholestasis. (increased sACE)

25 Vascular Pathologies Involving An Endothelial Abnormality:

Deep vein thrombosis, and in endothelium dysfunctions related to the toxicity of chemo- and radiotherapy used in cancers, leukemias, and hematopoietic or organ transplantations.

Thus the present invention provides by its first aspect, a novel isolated
30 nucleic acid molecule comprising or consisting of any one of the coding sequence

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SEQ ID NO: 1 to SEQ ID NO: 87, fragments of said coding sequence having at least 20 nucleic acids (provided that said fragments are continuous stretches of nucleotides not present in the original sequence from which the variant was varied), or a molecule comprising a sequence having at least 90% identity to SEQ ID NO: 1 to SEQ ID NO: 87, provided that the molecule is not completely identical to the original sequence from which the variant was varied. In particular, the above variant is that of SEQ ID NO: 57 or SEQ ID NO: 85 being the ACEV nucleic acid sequence.

The present invention further provides a protein or polypeptide comprising or consisting of an amino acid sequence encoded by any of the above nucleic acid sequences, termed herein "*variant product*", for example, an amino acid sequence having the sequence as depicted in any one of SEQ ID NO: 88 to SEQ ID NO: 174, fragments of the above amino acid sequence having a length of at least 10 amino acids coded by the above fragments of the nucleic acid sequences, as well as homologues of the above amino acid sequences in which one or more of the amino acid residues has been substituted (by conservative or non-conservative substitution) added, deleted, or chemically modified. In particular, the product is the amino acid sequence of the ACEV as depicted in SEQ ID NO: 144 or 172.

The deletions, insertions and modifications should be in regions, or adjacent to regions, wherein the variant differs from the original sequence.

For example, where the variant is different from the original sequence by addition of a short stretch of 10 amino acids, in the terminal or non-terminal portion of the peptide, the invention also concerns homologues of that variant where the additional short stretch is altered for example, it includes only 8 additional amino acids, includes 13 additional amino acids, or it includes 10 additional amino acids, however some of them being conservative or non-conservative substitutes of the original additional 10 amino acids of the novel variants. In all cases the changes in the homolog, as compared to the original sequence, are in the same regions where the variant differs from the original sequence, or in regions adjacent to said region.

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Another example is where the variant lacks a non-terminal region (for example of 20 amino acids) which is present in the original sequence (due for example to exon exclusion). The homologues may lack in the same region only 17 amino acids or 23 amino acids. Again the deletion is in the same region where the
5 variant lacks a sequence as compared to the original sequence, or in a region adjacent thereto.

It should be appreciated that once a man versed in the art's attention is directed to the importance of a specific region, due to the fact that this region differs in the variant as compared to the original sequence, there is no problem in
10 derivating said specific region by addition to it, deleting from it, or substituting some amino acids in it. Thus homologues of variants which are derivated from the variant by changes (deletion, addition, substitution) only in said region as well as in regions adjacent to it are also a part of the present invention. Generally, if the variant is distinguished from the original sequence by some sort of physiological
15 activity, then the homolog is distinguished from the original sequence in essentially the same manner.

The present invention further provides nucleic acid molecule comprising or consisting of a sequence which encodes the above amino acid sequences, (including the fragments and homologues of the amino acid sequences and in
20 particular the ACEV amino acid sequence). Due to the degenerative nature of the genetic code, a plurality of alternative nucleic acid, beyond those depicted in any one of SEQ ID NO: 1 to SEQ ID NO: 87, can code for the amino acid sequence of the invention. Those alternative nucleic acid sequences which code for the same amino acid sequences codes by the sequence SEQ ID NO: 1 to SEQ ID NO: 87 are
25 also an aspect of the of the present invention.

The present invention further provides expression vectors and cloning vectors comprising any of the above nucleic acid sequences, as well as host cells transfected by said vectors.

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The present invention still further provides pharmaceutical compositions comprising, as an active ingredient, said nucleic acid molecules, said expression vectors, or said protein or polypeptide.

These pharmaceutical compositions are suitable for the treatment of diseases
5 and pathological conditions, which can be ameliorated or cured by raising the level of any one of the variant products of the invention. In particular, those diseases are diseases which are associated with malfunction or under function of the original sequence (for example, given in the "Detailed Description" part of the specification). Thus for example, SEQ ID NO: 3 and sequences encoded thereby
10 may be used to treat diseases associated with coagulation of blood.

By a second aspect, the present invention provides a nucleic acid molecule comprising or consisting of a non-coding sequence which is complementary to that of any one of SEQ ID NO: 1 to SEQ ID NO: 87, or complementary to a sequence having at least 90% identity to said sequence (with the proviso added above) or a
15 fragment of said two sequences (according to the above definition of fragment). The complementary sequence may be a DNA sequence which hybridizes with any one of SEQ of ID NO: 1 to SEQ ID NO: 87 or hybridizes to a portion of that sequence having a length sufficient to inhibit the transcription of the complementary sequence. The complementary sequence may be a DNA sequence
20 which can be transcribed into an mRNA being an antisense to the mRNA transcribed from any one of SEQ ID NO: 1 to SEQ ID NO: 87 or into an mRNA which is an antisense to a fragment of the mRNA transcribed from any one of SEQ ID NO: 1 to SEQ ID NO: 87 which has a length sufficient to hybridize with the mRNA transcribed from SEQ ID NO: 1 to SEQ ID NO: 87, so as to inhibit its
25 translation. The complementary sequence may also be the mRNA or the fragment of the mRNA itself.

The nucleic acids of the second aspect of the invention may be used for therapeutic or diagnostic applications for example as probes used for the detection of the variants of the invention. The presence of the variant transcript or the level of
30 the variant transcript may be indicative of a multitude of diseases, disorders and

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various pathological as well as normal conditions for example, as indicated above for the variants in general, and for the ACEV in particular. In addition or alternatively, the ratio of the level of the transcripts of the variants of the invention may also be compared to that of the transcripts of the original sequences from
5 which have been varied, or to the level of transcript of other variants, and said ratio may be indicative to a multitude of diseases, disorders and various pathological and normal conditions.

The present invention also provides expression vectors comprising any one of the above defined complementary nucleic acid sequences and host cells
10 transfected with said nucleic acid sequences or vectors, being complementary to those specified in the first aspect of the invention.

The invention also provides anti-variant product antibodies, namely antibodies directed against the variant product which specifically bind to said variant product. Said antibodies are useful both for diagnostic and therapeutic
15 purposes. For example said antibody may be as an active ingredient in a pharmaceutical composition as will be explained below.

The present invention also provides pharmaceutical compositions comprising, as an active ingredient, the nucleic acid molecules which comprise or consist of said complementary sequences, or of a vector comprising said
20 complementary sequences. The pharmaceutical composition thus provides pharmaceutical compositions comprising, as an active ingredient, said anti-variant product antibodies.

The pharmaceutical compositions comprising said anti-variant product antibodies or the nucleic acid molecule comprising said complementary sequence,
25 are suitable for the treatment of diseases and pathological conditions where a therapeutically beneficial effect may be achieved by neutralizing the variant (either at the transcript or product level) or decreasing the amount of the variant product or blocking its binding to its target, for example, by the neutralizing effect of the antibodies, or by the effect of the antisense mRNA in decreasing the expression
30 level of the variant sequence.

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Examples of diseases which can be treated either with ACEV sequence, an expression vector comprising that sequence, a sequence complementary to the ACEV sequence, an expression vector comprising said complementary sequence, ACEV product or an antibody to the product is any one of the diseases mentioned
5 in connection with the detection aspect above.

According to the third aspect of the invention the present invention provides methods for detecting the level of the transcript (mRNA) of said variant product in a body fluid sample, or in a specific tissue sample, for example by use of probes comprising or consisting of said coding sequences; as well as methods for detecting
10 levels of expression of said product in tissue, e.g. by the use of antibodies capable of specifically reacting with the variant products of the invention. Detection of the level of the expression of the variant of the invention in particular as compared to that of the original sequence from which it was varied or compared to other variant sequences all varied from the same original sequence may be indicative of a
15 plurality of physiological or pathological conditions. A preferred example is the detection of ACEV nucleic acid sequence, ACEV product or anti-ACEV antibody.

The method, according to this latter aspect, for detection of a nucleic acid sequence which encodes the variant product in a biological sample, comprises the steps of:

- 20 (a) providing a probe comprising at least one of the nucleic acid sequences defined above;
- (b) contacting the biological sample with said probe under conditions allowing hybridization of nucleic acid sequences thereby enabling formation of hybridization complexes;
- 25 (c) detecting hybridization complexes, wherein the presence of the complexes indicates the presence of nucleic acid sequence encoding the variant product in the biological sample.

The method as described above is qualitative, i.e. indicates whether the transcript is present in or absent from the sample. The method can also be
30 quantitative, by determining the level of hybridization complexes and then

calibrating said levels to determining levels of transcripts of the desired variant in the sample.

Both qualitative and quantitative determination methods can be used for diagnostic, prognostic and therapy planning purposes.

5 By a preferred embodiment the probe is part of a nucleic acid chip used for detection purposes, i.e. the probe is a part of an array of probes each present in a known location on a solid support.

The nucleic acid sequence used in the above method may be a DNA sequence an RNA sequence, etc; it may be a coding or a sequence or a sequence
10 complementary thereto (for respective detection of RNA transcripts or coding-DNA sequences). By quantization of the level of hybridization complexes and calibrating the quantified results it is possible also to detect the level of the transcript in the sample.

Methods for detecting mutations in the region coding for the variant product
15 are also provided, which may be methods carried-out in a binary fashion, namely merely detecting whether there is any mismatches between the normal variant nucleic acid sequence of the invention and the one present in the sample, or carried-out by specifically detecting the nature and location of the mutation.

The present invention also concerns a method for detecting variant product
20 in a biological sample, comprising the steps of:

(a) contacting with said biological sample the antibody of the invention, thereby forming an antibody-antigen complex; and

(b) detecting said antibody-antigen complex

wherein the presence of said antibody-antigen complex correlates with the
25 presence of variant product in said biological sample.

Many diseases are diagnosed by detecting the presence of antibodies against a protein characterizing the disease in the blood, serum or any other body fluid of the patient. The present invention also concerns a method for detecting anti-variant antibody in a biological sample, comprising:

- 20 -

(a) contacting said sample with the variant product of the invention, thereby forming an antibody-antigen complex; and

(b) detecting said antibody-antigen complex

wherein the presence of said antibody-antigen complex correlates with the
5 presence of anti-variant antibody in the sample.

As indicated above, both methods (for detection of variant product and for detection of the anti-variant antibody) can be quantitized to determine the level or the amount of the variant or antibody in the sample, alone or in comparison to the level of the original amino acid sequence from which it was varied or compared to
10 the level of antibodies against the original amino acid sequence, and qualitative and quantitative results may be used for diagnostic, prognostic and therapy planning purposes.

The invention also concerns distinguishing antibodies, i.e. antibodies capable of binding either to the variant product or to the original sequence from
15 which the variant has been varied, while not binding to the original sequence or the variant product respectively. These distinguishing antibodies may be used for detection purposes.

By yet another aspect the invention also provides a method for identifying candidate compounds capable of binding to the variant product and modulating its
20 activity (being either activators or deactivators). The method includes:

(i) providing a protein or polypeptide comprising an amino acid sequence substantially as depicted in any one of SEQ ID NO: 88 to 174, or a fragment of such a sequence;

(ii) contacting a candidate compound with said amino acid sequence;

25 (iii) measuring the physiological effect of said candidate compound on the activity of the amino acid sequences and selecting those compounds which show a significant effect on said physiological activity.

The present invention also concerns compounds identified by the above methods described above, which compound may either be an activator of the
30 variant product or a deactivator thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

In order to understand the invention and to see how it may be carried out in practice, a preferred embodiment will now be described, by way of non-limiting example only, with reference to the accompanying drawings, in which:

5 **Fig. 1** is a comparison between the amino acid sequence of SEQ ID NO: 88 and the original sequence from which it has been varied;

Fig. 2 is a comparison between the amino acid sequence of SEQ ID NO: 89 and the original sequence from which it has been varied;

Fig. 3 is a comparison between the amino acid sequence of SEQ ID NO: 90
10 and the original sequence from which it has been varied;

Fig. 4 is a comparison between the amino acid sequence of SEQ ID NO: 91 and the original sequence from which it has been varied;

Fig. 5 is a comparison between the amino acid sequence of SEQ ID NO: 92 and the original sequence from which it has been varied;

15 **Fig. 6** is a comparison between the amino acid sequence of SEQ ID NO: 93 and the original sequence from which it has been varied;

Fig. 7 is a comparison between the amino acid sequence of SEQ ID NO: 94 and the original sequence from which it has been varied;

Fig. 8 is a comparison between the amino acid sequence of SEQ ID NO: 95
20 and the original sequence from which it has been varied;

Fig. 9 is a comparison between the amino acid sequence of SEQ ID NO: 96 and the original sequence from which it has been varied;

Fig. 10 is a comparison between the amino acid sequence of SEQ ID NO: 97 and the original sequence from which it has been varied;

25 **Fig. 11** is a comparison between the amino acid sequence of SEQ ID NO: 98 and the original sequence from which it has been varied;

Fig. 12 is a comparison between the amino acid sequence of SEQ ID NO: 99 and the original sequence from which it has been varied;

Fig. 13 is a comparison between the amino acid sequence of SEQ ID
30 NO: 100 and the original sequence from which it has been varied;

Fig. 14 is a comparison between the amino acid sequence of SEQ ID NO: 101 and the original sequence from which it has been varied;

Fig. 15 is a comparison between the amino acid sequence of SEQ ID NO: 102 and the original sequence from which it has been varied;

5 **Fig. 16** is a comparison between the amino acid sequence of SEQ ID NO: 103 and the original sequence from which it has been varied;

Fig. 17 is a comparison between the amino acid sequence of SEQ ID NO: 104 and the original sequence from which it has been varied;

10 **Fig. 18** is a comparison between the amino acid sequence of SEQ ID NO: 105 and the original sequence from which it has been varied;

Fig. 19 is a comparison between the amino acid sequence of SEQ ID NO: 106 and the original sequence from which it has been varied;

Fig. 20 is a comparison between the amino acid sequence of SEQ ID NO: 107 and the original sequence from which it has been varied;

15 **Fig. 21** is a comparison between the amino acid sequence of SEQ ID NO: 108 and the original sequence from which it has been varied;

Fig. 22 is a comparison between the amino acid sequence of SEQ ID NO: 109 and the original sequence from which it has been varied;

20 **Fig. 23** is a comparison between the amino acid sequence of SEQ ID NO: 110 and the original sequence from which it has been varied;

Fig. 24 is a comparison between the amino acid sequence of SEQ ID NO: 111 and the original sequence from which it has been varied;

Fig. 25 is a comparison between the amino acid sequence of SEQ ID NO: 112 and the original sequence from which it has been varied;

25 **Fig. 26** is a comparison between the amino acid sequence of SEQ ID NO: 113 and the original sequence from which it has been varied;

Fig. 27 is a comparison between the amino acid sequence of SEQ ID NO: 114 and the original sequence from which it has been varied;

30 **Fig. 28** is a comparison between the amino acid sequence of SEQ ID NO: 115 and the original sequence from which it has been varied;

Fig. 29 is a comparison between the amino acid sequence of SEQ ID NO: 116 and the original sequence from which it has been varied;

Fig. 30 is a comparison between the amino acid sequence of SEQ ID NO: 117 and the original sequence from which it has been varied;

5 Fig. 31 is a comparison between the amino acid sequence of SEQ ID NO: 118 and the original sequence from which it has been varied;

Fig. 32 is a comparison between the amino acid sequence of SEQ ID NO: 119 and the original sequence from which it has been varied;

10 Fig. 33 is a comparison between the amino acid sequence of SEQ ID NO: 120 and the original sequence from which it has been varied;

Fig. 34 is a comparison between the amino acid sequence of SEQ ID NO: 121 and the original sequence from which it has been varied;

Fig. 35 is a comparison between the amino acid sequence of SEQ ID NO: 122 and the original sequence from which it has been varied;

15 Fig. 36 is a comparison between the amino acid sequence of SEQ ID NO: 123 and the original sequence from which it has been varied;

Fig. 37 is a comparison between the amino acid sequence of SEQ ID NO: 124 and the original sequence from which it has been varied;

20 Fig. 38 is a comparison between the amino acid sequence of SEQ ID NO: 125 and the original sequence from which it has been varied;

Fig. 39 is a comparison between the amino acid sequence of SEQ ID NO: 126 and the original sequence from which it has been varied;

Fig. 40 is a comparison between the amino acid sequence of SEQ ID NO: 127 and the original sequence from which it has been varied;

25 Fig. 41 is a comparison between the amino acid sequence of SEQ ID NO: 128 and the original sequence from which it has been varied;

Fig. 42 is a comparison between the amino acid sequence of SEQ ID NO: 129 and the original sequence from which it has been varied;

30 Fig. 43 is a comparison between the amino acid sequence of SEQ ID NO: 130 and the original sequence from which it has been varied;

Fig. 44 is a comparison between the amino acid sequence of SEQ ID NO: 131 and the original sequence from which it has been varied;

Fig. 45 is a comparison between the amino acid sequence of SEQ ID NO: 132 and the original sequence from which it has been varied;

5 **Fig. 46** is a comparison between the amino acid sequence of SEQ ID NO: 133 and the original sequence from which it has been varied;

Fig. 47 is a comparison between the amino acid sequence of SEQ ID NO: 134 and the original sequence from which it has been varied;

Fig. 48 is a comparison between the amino acid sequence of SEQ ID
10 NO: 135 and the original sequence from which it has been varied;

Fig. 49 is a comparison between the amino acid sequence of SEQ ID NO: 136 and the original sequence from which it has been varied;

Fig. 50 is a comparison between the amino acid sequence of SEQ ID NO: 137 and the original sequence from which it has been varied;

15 **Fig. 51** is a comparison between the amino acid sequence of SEQ ID NO: 138 and the original sequence from which it has been varied;

Fig. 52 is a comparison between the amino acid sequence of SEQ ID NO: 139 and the original sequence from which it has been varied;

Fig. 53 is a comparison between the amino acid sequence of SEQ ID NO:
20 140 and the original sequence from which it has been varied;

Fig. 54 is a comparison between the amino acid sequence of SEQ ID NO: 141 and the original sequence from which it has been varied;

Fig. 55 is a comparison between the amino acid sequence of SEQ ID NO: 142 and the original sequence from which it has been varied;

25 **Fig. 56** is a comparison between the amino acid sequence of SEQ ID NO: 143 and the original sequence from which it has been varied;

Fig. 57 is a comparison between the amino acid sequence of SEQ ID NO: 144 and the original sequence from which it has been varied;

Fig. 58 is a comparison between the amino acid sequence of SEQ ID NO:
30 145 and the original sequence from which it has been varied;

Fig. 59 is a comparison between the amino acid sequence of SEQ ID NO: 146 and the original sequence from which it has been varied;

Fig. 60 is a comparison between the amino acid sequence of SEQ ID NO: 147 and the original sequence from which it has been varied;

5 Fig. 61 is a comparison between the amino acid sequence of SEQ ID NO: 148 and the original sequence from which it has been varied;

Fig. 62 is a comparison between the amino acid sequence of SEQ ID NO: 149 and the original sequence from which it has been varied;

10 Fig. 63 is a comparison between the amino acid sequence of SEQ ID NO: 150 and the original sequence from which it has been varied;

Fig. 64 is a comparison between the amino acid sequence of SEQ ID NO: 151 and the original sequence from which it has been varied;

Fig. 65 is a comparison between the amino acid sequence of SEQ ID NO: 152 and the original sequence from which it has been varied;

15 Fig. 66 is a comparison between the amino acid sequence of SEQ ID NO: 153 and the original sequence from which it has been varied;

Fig. 67 is a comparison between the amino acid sequence of SEQ ID NO: 154 and the original sequence from which it has been varied;

20 Fig. 68 is a comparison between the amino acid sequence of SEQ ID NO: 155 and the original sequence from which it has been varied;

Fig. 69 is a comparison between the amino acid sequence of SEQ ID NO: 156 and the original sequence from which it has been varied;

Fig. 70 is a comparison between the amino acid sequence of SEQ ID NO: 157 and the original sequence from which it has been varied;

25 Fig. 71 is a comparison between the amino acid sequence of SEQ ID NO: 158 and the original sequence from which it has been varied;

Fig. 72 is a comparison between the amino acid sequence of SEQ ID NO: 159 and the original sequence from which it has been varied;

30 Fig. 73 is a comparison between the amino acid sequence of SEQ ID NO: 160 and the original sequence from which it has been varied;

Fig. 74 is a comparison between the amino acid sequence of SEQ ID NO: 161 and the original sequence from which it has been varied;

Fig. 75 is a comparison between the amino acid sequence of SEQ ID NO: 162 and the original sequence from which it has been varied;

5 **Fig. 76** is a comparison between the amino acid sequence of SEQ ID NO: 163 and the original sequence from which it has been varied;

Fig. 77 is a comparison between the amino acid sequence of SEQ ID NO: 164 and the original sequence from which it has been varied;

Fig. 78 is a comparison between the amino acid sequence of SEQ ID NO: 10 165 and the original sequence from which it has been varied;

Fig. 79 is a comparison between the amino acid sequence of SEQ ID NO: 166 and the original sequence from which it has been varied;

Fig. 80 is a comparison between the amino acid sequence of SEQ ID NO: 167 and the original sequence from which it has been varied;

15 **Fig. 81** is a comparison between the amino acid sequence of SEQ ID NO: 168 and the original sequence from which it has been varied;

Fig. 82 is a comparison between the amino acid sequence of SEQ ID NO: 169 and the original sequence from which it has been varied;

Fig. 83 is a comparison between the amino acid sequence of SEQ ID NO: 20 170 and the original sequence from which it has been varied;

Fig. 84 is a comparison between the amino acid sequence of SEQ ID NO: 171 and the original sequence from which it has been varied;

Fig. 85 is a comparison between the amino acid sequence of SEQ ID NO: 172 and the original sequence from which it has been varied;

25 **Fig. 86** is a comparison between the amino acid sequence of SEQ ID NO: 173 and the original sequence from which it has been varied;

Fig. 87 is a comparison between the amino acid sequence of SEQ ID NO: 174 and the original sequence from which it has been varied;

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Fig. 88 shows immunohistochemical staining with antibodies against a fragment of the ACEV product of SEQ ID NO: 144; expressed in ductal epitilus in salivatory gland (magnification X 100);

Fig. 89 shows the same as in Fig. 89 (magnification X 400);

5 Fig. 90 shows immunohistochemical staining with antibodies against a fragment of ACEV product of SEQ ID NO: 144 expressed in salivary glands surrounding the lymph nodes; and

Fig. 91 shows RT-PCR results of the ACEV sequence expressed in salivary glands.

10

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

Example I: Comparison of variants with original sequences

Original sequences were obtained from GenBank Version 110. Comparison between the original sequences and the novel variant sequences was
15 made using the Pileup application from the GCG suite version 10.0 (January 1999), with the default values:

Gap creation penalty (GapWeight): 8

Gap extension penalty (GapLengthWeight): 2

The comparison is shown in Fig. 1 to 87 which show the comparison of
20 each of the variant products depicted in SEQ ID NO: 88 to 174 with the original sequence from which it was varied.

The following is a list which gives the name and the description of each original sequence from which the alternative splice variant has been varied by alternative splicing. The description is followed by the internal reference to the
25 novel variant (NV-NV... or NV-... etc.) and a short comparison between the variant and the original sequence. It should be noticed that several splice variants may have been originated from the same parent sequence by several different alternative splicings. The following table summarizes the accession number of the original sequence, the terminology of the new variant (RN-NV... or NV-...) and
30 the description of the difference between the new variant and the original sequence.

Table

Accession	SEQ ID NO:	Description of the New Variant
AA2A_HUMAN	88	Gap between amino acids at the positions 237-247 of the original protein. Missing 6th transmembrane loop of the original Adenosine A2 receptor.
ASM_HUMAN	89	Insertion of 2 amino acids after amino acid at the position 34 and insertion of 54 amino acids after amino acid at the position 492 of the original SPHINGOMYELIN PHOSPHODIESTERASE protein.
FA12_HUMAN	90	Alternative 10 C-terminal amino acids. Has part of catalytic domain missing 1 active site.
GCSR_HUMAN	91	Deletion of 62 amino acids between the positions 320-382 of the original GRANULOCYTE COLONY STIMULATING FACTOR receptor. The deletion is in the EXTRACELLULAR domain in one of the FIBRONECTIN TYPE-III domains R1.
GCSR_HUMAN	92	Insertion of 37 amino acids in the extracellular domain after the position 574 of the original GRANULOCYTE COLONY STIMULATING FACTOR receptor.
GLR2_HUMAN	93	Replacement of 88 C-terminal amino acids of the original glutamate receptor 2 by alternative 42 amino acids. Has most of domains, might be missing 4th transmembrane domain.
GLUC_HUMAN	94	Gap; 156aa compared to 180aa; exact 1-108; gap 108-132; exact 132-180. Missing almost whole GLUCAGON-LIKE PEPTIDE 1
IHBA_HUMAN	95	Replacement of 128 N-terminal amino acids of the original inhibin protein by alternative 5 amino acids. The deleted part contains propep and glycosylation site of the original protein. The resulting new variant sustains the inhibin beta chain.
IL6_HUMAN	96	Deletion of 17 amino acids between the positions 79-96 of the original interleukin 6 protein. Has all necessary domains.
IL6_HUMAN	97	Deletion of 55 amino acids between the positions 6-61 of the original protein. Has only the beginning of signal peptide; has disulfide bonds and carbohydrate region.
REL1_HUMAN	98	Insertion of 35 amino acids after the amino acid

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		at the position 70 of the original relaxin protein. The insertion is in the connecting peptide.
SY04_HUMAN	99	Deletion of 5 amino acids between the positions 65-69 of the original protein. Replacement of the amino acid at the position 70 of the original protein by an alternative amino acid. Missing part of strand.
TSP1_HUMAN	100	Truncated: exact 1-722 (731aa long compared to 1170aa), last 9 amino acids are different. Missing 7 X TSP TYPE-3-REPEATS CA-BINDING domain C-TERMINAL, missing CELL ATTACHMENT SITE, missing 1 out of 4 glycosylation sites. Has all other components including signal peptide.
TSP1_HUMAN	101	Truncated exact 1-548 (555aa long compared to 1170) last 7aa different. Missing 3 X EGF-TYPE REPEATS, missing 7 X TSP TYPE-3 REPEATS Ca-BINDING domain C-TERMINAL missing CELL ATTACHMENT SITE, missing all diSulfide bonds, missing 2 out of 4 glycosylation sites. Has all other domains (including signal peptide).
TSP1_HUMAN	102	Truncated: exact 1-490 (546aa long compared to 1170) last 56 amino acids are different. Missing 1 out of 3 X TXP TYPE-1 REPEATS (CS-LIKE), Missing 3 X EGF-TYPE REPEATS, missing 7 X TSP TYPE-3 REPEATS CA-BINDING domain C-TERMINAL missing CELL ATTACHMENT SITE, missing all diSulfide bonds, missing 2 out of 4 glycosylations. Has all other domains (including signal peptide).
TSP1_HUMAN	103	Truncated: exact 1-431aa (459aa long compared to 1170) last 28 amino acids are different. Missing 2 out of 3 X TSP TYPE-1 REPEATS (CS-LIKE), Missing 3 X EGF-TYPE REPEATS, missing 7 X TSP TYPE-3 REPEATS CA-BINDING domain C-TERMINAL missing CELL ATTACHMENT SITE, missing all disulfide bonds, missing 2 out of 4 glycosylations. Has all other domains (including signal peptide).
TYPH_HUMAN	104	Deletion of 119 amino acids between the positions 33-452 of the original protein. The resulting new variant is missing the 3 rd repeat of the original protein.

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TYPH_HUMAN	105	Replacement of 48 amino acids between the positions 216-264 of the original protein by alternative 9 amino acids.
TYPH_HUMAN	106	Deletion of 119 amino acids between the positions 333-452, missing 3 rd repeat of the original protein. Replacement of 48 amino acids between the positions 216-264 of the original protein by alternative 9 amino acids.
IC1_HUMAN	107	Deletion of 19 amino acids between the positions 29-48 of the original protein. Missing 1 glycosylation out of 14.
PT16_HUMAN	108	Deletion of 261 N-terminal amino acids of the original protein (the first possible Met is at the position 261). The new variant has 116 amino acids compared to 376 in the original protein (exact 261-376), including the active site.
PT16_HUMAN	109	Deletion of 57 amino acids between the positions 267-325 of the original protein. The resulting new variant contains the active site.
PT16_HUMAN	110	Deletion of 189 amino acids between the positions 89-278 of the original protein. The resulting new variant contains the active site.
PT16_HUMAN	111	Replacement of 376 C-terminal amino acids of the original protein by alternative 5 amino acids. The resulting new variant doesn't contain the active site.
IAP2_HUMAN	112	Truncated: 305 amino acids compared to 618 aa (protein 2). The new variant contains exact positions 1-299, last 6 amino acids are different. Two SNIPs in position 235 and 241 of the original protein. The new variant is missing Zn Finger and half of 3 rd BIR repeat.
SET_HUMAN	113	Extra 83 amino acids in the N-terminus of the protein. The added sequence has predicted potential transmembrane domain (probable signal peptide?)
SET_HUMAN	114	Replacement of 24 C-terminal amino acids of the original protein by alternative 8 amino acids. Missing part of ASP/GLU-RICH and BREAKPOINT FOR TRANSLOCATION TO FORM SET-CAN ONCOGENE.
CDNC_HUMAN	115	Deletion of 178 amino acids at the positions 97-275 of the original protein. Insertion of 121 amino acids at the N-terminus. The resulting new variant is missing PAPA repeats.
F13B_MOUSE	116	Deletion of 87 C-terminal amino acids of the original protein. SNIP at position 236 (L->V). The resulting new variant is missing the last

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		shushi repeat.
EGF_MOUSE	117	Deletion of 641 amino acids between the positions 67-708 of the original protein. Missing 4 EGF-like domains, 2 glycosylations, 9 diSulfide bonds.
EGF_MOUSE	118	Deletion of 641 amino acids between the positions 67-708, and deletion of 45 amino acids between the positions 1020-1065 of the original protein. Missing 4 EGF-like domains, 2 glycosylations, 9 diSulfide bonds. Missing transmembrane domain.
EGF_MOUSE	119	Deletion of 641 amino acids between the positions 67-708 of the original protein. Missing 4 EGF-like domains, 2 glycosylations, 9 diSulfide bonds. Replacement of 419 C-terminal amino acids by 5 amino acids.
EGF_MOUSE	120	Deletion of 841 amino acids between the positions 18-859 of the original protein. Missing 5 EGF-like domains and 2 glycosylation sites.
EGF_MOUSE	121	Deletion of 774 amino acids between the positions 5-779 of the original protein. Missing signal peptide, 5 EGF-like domains, and 2 glycosylation sites.
P53_MOUSE	122	Deletion of 336 N-terminal amino acids of the original protein. Missing ASP/GLU-RICH (ACIDIC), missing hydrophobic domain, missing NUCLEAR LOCALIZATION SIGNAL, missing 1 out of 2 PHOSPHORYLATION sites.
NME3_HUMAN	123	Deletion of 381 N-terminal amino acids of the original protein. Missing 2 out of 4 glycosylation sites.
TRFE_HUMAN	124	Deletion of 34 amino acids between the positions 654-689 of the original protein. Loss of disulfide bond.
TRFE_HUMAN	125	Deletion of 52 amino acids between the positions 447-499 of the original protein. Loss of disulfide bond.
BAA23795	126	Replacement of 83 C-terminal amino acids from probable cytoplasmic domain of the original protein by alternative 4 amino acids. Resulting in truncated new variant: 4787 compared to 4866, exact 1-4783 with last 4 amino acids different.
VIPS_HUMAN	127	Replacement of 64 C-terminal amino acids of the original protein by alternative 7 amino acids. The resulting new variant is missing the

		last transmembrane and the cytoplasmic domains.
PACR_HUMAN	128	Deletion of 22 amino acids between the positions 88-110 of the original protein. The deletion is an extracellular loop.
NRP_HUMAN	129	Deletion of 540 C-terminal amino acids of the original protein, resulting in truncated new variant (383 compared to 923 amino acids). The new variant is missing part of the extracellular domain, the cytoplasmic and the transmembrane domains.
NRP_HUMAN	130	Replacement of 595 C-terminal amino acids of the original protein by alternative 11 amino acids. The resulting new variant is truncated (339 compared to 923 amino acids, exact 1-328 with last 11 amino acids different), and is missing part of the extracellular domain, the cytoplasmic and the transmembrane domains.
gi 1899200	131	Deletion of 114 amino acids between the positions 1257-1372 of the original N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2A protein.
VIPS_HUMAN	132	Replacement of 56 C-terminal amino acids from the cytoplasmic domain of the original protein by alternative 73 amino acids.
VIPS_HUMAN	133	Replacement of 56 C-terminal amino acids from the cytoplasmic domain of the original protein by alternative 70 amino acids.
IG1R_HUMAN	134	Deletion of 22 amino acids between the positions 1268-1291 of the original protein. The deleted fragment is part of the cytoplasmic domain of INSULIN-LIKE GROWTH FACTOR I RECEPTOR, BETA-CHAIN.
NRP_HUMAN	135	Replacement of 282 C-terminal amino acids of the original protein, including the transmembrane domain and the MAM domain, by alternative 3 amino acids.
NRP_HUMAN	136	Deletion of 83 amino acids between the positions 538-622 of the original protein. The deleted region includes part of the F5/8 TYPE C 2 domain and part of the MAM domain.
NRP_HUMAN	137	Deletion of 385 C-terminal amino acids of the original protein, including the transmembrane domain and the MAM domain.
FGR3_HUMAN	138	Replacement of 496 C-terminal amino acids of the original protein by alternative 79 amino acids.. The deleted region includes the C-terminal part of the extracellular domain, the

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		transmembrane domain, the cytoplasmic domain, the protein kinase domain and the two ATP binding domains.
F13B_MOUSE	139	Replacement of 340 aa of the c-terminus of the original protein in 3aa deletion of sushi 6-10 domain
EGF_MOUSE	140	Deletion of 144 amino acids between the positions 1020-1165, including the transmembrane domain and part of the cytoplasmic domain of the original protein.
EGF_MOUSE	141	Replacement of 418 C-terminal amino acids of the original protein by alternative 5 amino acids. The deleted region includes the EGF active chain, 4 out of 9 EGF-like domains within the extracellular region of the protein, the transmembrane and the cytoplasmic regions.
EGF_MOUSE	142	Deletion of 641 amino acids between the positions 66-707 of the original protein. The deleted region is in the extracellular part of the protein and it includes 4 out of 9 EGF-like domains. NV-20 contains the original signal peptide, part of the extracellular domain, the epidermal growth factor chain (located between the positions 977-1029 of the original protein), and the original transmembrane and the cytoplasmic domains.
EGF_MOUSE	143	Deletion of 842 amino acids between the positions 17-859 of the original protein (including replacement of the amino acid in the position 859 by an alternative one). The deleted region is in the extracellular part of the protein and it includes 5 out of 9 EGF-like domains. NV-20 contains the original signal peptide, part of the extracellular domain, the epidermal growth factor chain (located between the positions 977-1029 of the original protein), and the original transmembrane and the cytoplasmic domains.
ACE_MOUSE	144	Replacement of 77 C-terminal amino acids of the original protein, including the entire transmembrane and cytoplasmic domains, by alternative 14 amino acids.
ESR1_MOUSE	145	Replacement of 229 C-terminal amino acids of the original protein, including part of the steroid-binding domain, by alternative 12 amino acids.
FA7_MOUSE	146	Deletion of 101 amino acids, between the positions 119-220 of the original protein. The

		deleted region contains 74 amino acids from the C-terminal end of the factor VII light chain, and 26 amino acids from the N-terminal end of the factor VII heavy catalytic chain. The deleted region includes EGF-like 2 domain and the cleavage site (by factor XA, factor XIIA, factor IXA, or thrombin) of the original protein.
CAL0_MOUSE	147	Deletion of 33 amino acids, spanning the positions 18-50, between the signal and the calcitonin peptide in the original precursor protein.
Gi 2826776	148	Replacement of the last 7 C-terminal amino acids of the original protein by alternative 11 amino acids.
PTI6_HUMAN	149	Replacement of the last 4 C-terminal amino acids of the original protein by alternative 28 amino acids.
PTI6_HUMAN	150	Replacement of the last 16 C-terminal amino acids of the original protein by alternative 12 amino acids.
_RIN1_HUMAN	151	Replacement of 158 last C-terminal amino acids of the original protein by alternative 71 amino acids with probable transmembrane region.
CDNC_HUMAN	152	Addition of 121 amino acids at the N-terminus of the protein.
CDN2_HUMAN	153	Replacement of 5 amino acids at the positions 18, 24, 27, 30, 37 of the original protein by alternative amino acids. Replacement of last 4 C-terminal amino acids of the original protein by alternative 20 amino acids.
CDN5_HUMAN	154	Replacement of the last 6 C-terminal amino acids of the original protein by alternative 52 amino acids.
HEP2_HUMAN	155	Deletion of 150 amino acids, between the positions 334-485, of the original protein. The deleted region includes the reactive bond (the active site) of the original protein. NV-33 does contain the chemotactic activity domain, the glycosaminoglycan-binding site and the hirudin-like 2 x 11 AA approximate repeats, Asp/Glu rich.
TFP2_HUMAN	156	Replacement of 36 C-terminal amino acids of the original protein by alternative 12 amino acids. The deleted region includes part of the BPTI/KUNITZ inhibitor domain-3 and the poly-Lysine domain of the original protein.
TFP2_HUMAN	157	Deletion of 25 amino acids, between the positions 153-178 of the original protein, and

- 35 -

		replacement of the amino acid at the position 179 by alternative one. The deleted region includes the active site and part of the BPTI/KUNITZ inhibitor domain-3.
TFPI_HUMAN	158	Replacement of 95 C-terminal amino acids of the original protein, containing the entire BPTI/KUNITZ inhibitor-3 domain, by alternative 16 amino acids.
IC1_HUMAN	159	Insertion of 136 aa at position 227 of the original protein.
PTI6_HUMAN	160	Replacement of last 15 aa in the original protein in 28 aa, the cds of the NV has no stop codon.
PTI6_HUMAN	161	Replacement of last 185 aa of the original protein in 13 aa. The NV lacks the ACT site.
PTI6_HUMAN	162	Replacement of last 230 aa of the original protein in 10 aa. The NV lacks the ACT site.
TYPH_HUMAN	163	Insertion of 35 aa at position 387 of the original protein.
CDNC_HUMAN	164	Replacement of 220 aa of the c-terminus of the original protein in 47 aa. Deletion of all 9 x 4 aa repeats of p-a-p-a. Deletion of the potential nuclear localization signal (278-281 in the original protein).
FGR3_HUMAN	165	Replacement of 264 aa of the c-terminus of the original protein in 19 aa. Deletion of part of the potential cytoplasmatic protein (397-806 in the original protein), part of the protein kinase domain (472-761), deletion of the ACT site (617).
TFP2_HUMAN	166	Replacement of 58 aa of the c-terminus of the original protein in 12 aa. Deletion of part of the bpti/kunitz inhibitor 3 domain (158-208 in the original protein).
TRFE_HUMAN	167	Insertion of 32 aa at position 366 of the original protein.
VIPS_HUMAN	168	Replacement of 388 aa of the c-terminus of the original protein in 27 aa. Deletion of all potential 7 trans membrana domain.
TFPI_HUMAN	169	Replacement of 180 aa of the n-terminus of the original protein in 37 aa. Deletion of the signal peptide and deletion of the bpti/kunitz inhibitor 1 and 2 domains.
P53_MOUSE	170	Replacement of 246 aa of the n-terminus of

- 36 -

		the original protein in 13 aa. Deletion of the asp/glu-rich (acidic) domain.
P53_MOUSE	171	Replacement of 246 aa of the n-terminus of the original protein in 13 aa. Deletion of the asp/glu-rich (acidic) domain.
ACE_MOUSE	172	Replacement of 77 aa of the c-terminus of the original protein in 17 aa. Deletion of the entire transmembrane and cytoplasmatic domains.
ESR1_MOUSE	173	Deletion of 225 aa of the c-terminus of the original protein. Deletion of most of the steroid binding domain (315-599 in the original protein). RT-PCR results implies that the NV exhibits similarity to thr somatic ACE (results not shown).
vesicular GABA and glycine transporter (mouse), gi 2826776	174	Replacement of 73 aa of the c-terminus of the original protein in 21 aa.

**Identification of the original sequence from which the novel
Variant was variant**

5

The following is the explanation of the definition to be used in the following:

- Accession:** Accession number of the original sequence in the GeneBank database
- Name:** Name of the original sequence in the database
- Function:** Physiological activity.

15

SEQ ID NO : Sequence number of variant

Description: the difference between the variant and the original sequence.

- Accession:** AA2A_HUMAN
- Name:** Adenosine A2 receptor
- Function:** Receptor for adenosine.

20

SEQ ID 1

- 37 -

Description: Gap between amino acids at the positions 237-247 of the original protein. Missing 6th transmembrane loop of the original Adenosine A2 receptor.

5 **Accession:** ASM_HUMAN
Name: SPHINGOMYELIN PHOSPHODIESTERASE
Function: Converts sphingomyelin to ceramide.

SEQ ID : 2

10

Description: Insertion of 2 amino acids after amino acid at the position 34 and insertion of 54 amino acids after amino acid at the position 492 of the original SPHINGOMYELIN PHOSPHODIESTERASE protein.

15 **Accession:** FA12_HUMAN
Name: COAGULATION FACTOR XII
Function: Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin.

20

SEQ ID : 3

Description: Alternative 10 C-terminal amino acids. Has part of catalytic domain missing 1 active site.

25

Accession: GCSR_HUMAN
Name: GRANULOCYTE COLONY STIMULATING FACTOR receptor
Function: Receptor for granulocyte colony-stimulating factor (g- csf).
30 In addition it may function in some adhesion or recognition events at the cell surface.

SEQ ID : 4

35 **Description:** Deletion of 62 amino acids between the positions 320-382 of the original GRANULOCYTE COLONY STIMULATING FACTOR receptor.

- 38 -

The deletion is in the EXTRACELLULAR domain in one of the FIBRONECTIN TYPE-III domains R1.

Accession: GCSR_HUMAN

5 **Name:** GRANULOCYTE COLONY STIMULATING FACTOR
receptor

Function: Receptor for granulocyte colony-stimulating factor (g- csf).
In addition it may function in some adhesion or recognition
events at the cell surface.

10

SEQ ID : 5

Description: Insertion of 37 amino acids in the extracellular domain after the
position 574 of the original GRANULOCYTE COLONY STIMULATING
15 **FACTOR** receptor.

Accession: GLR2_HUMAN

Name: Glutamate receptor 2

20 **Function:** L-glutamate acts as an excitatory neurotransmitter at many
synapses in the central nervous system. the postsynaptic
actions of Glu are mediated by a variety of receptors are
named according to their selective agonists

SEQ ID : 6

25

Description: Replacement of 88 C-terminal amino acids of the original
glutamate receptor 2 by alternative 42 amino acids. Has most of domains, might
be missing 4th transmembrane domain.

30 **Accession:** GLUC_HUMAN

Name: Glucagon

Function: Promotes hydrolysis of glycogen and lipids, and raises the
blood sugar level.

35 **SEQ ID : 7**

- 39 -

Description Gap; 156aa compared to 180aa; exact 1-108; gap 108-132; exact 132-180. Missing almost whole GLUCAGON-LIKE PEPTIDE 1

Accession: IHBA_HUMAN

5 **Name:** Inhibin; erythroid differentiation factor

Function: Inhibin is a gonadal glycopeptide that inhibits the secretion of follitropin by the pituitary gland. On the other hand activin activates the secretion of follitropin. Activin is also important in embryonic axial development.

10

SEQ ID : 8

Description: Replacement of 128 N-terminal amino acids of the original inhibin protein by alternative 5 amino acids. The deleted part contains propep and
15 glycosylation site of the original protein. The resulting new variant sustains the inhibin beta chain.

Accession: IL6_HUMAN

Name: Interleukin 6

20 **Function:** IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation.

25 **SEQ ID : 9**

Description: Deletion of 17 amino acids between the positions 79-96 of the original interleukin 6 protein. Has all necessary domains.

30 **Accession:** IL6_HUMAN

Name: Interleukin 6

Function: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma
35 and plasmacytoma growth, it induces nerve cells differentiation.

- 40 -

SEQ ID : 10

Description: Deletion of 55 amino acids between the positions 6-61 of the original protein. Has only the beginning of signal peptide; has disulfide bonds and carbohydrate region.

Accession: REL1_HUMAN

Name: Relaxin

Function: Relaxin is an ovarian hormone that acts with estrogen to produce dilatation of the birth canal in many mammals.

SEQ ID : 11

Description: Insertion of 35 amino acids after the amino acid at the position 70 of the original relaxin protein. The insertion is in the connecting peptide.

Accession: SY04_HUMAN

Name: SMALL INDUCIBLE CYTOKINE A4, MACROPHAGE INFLAMMATORY PROTEIN 1-BETA

Function: Monokine with inflammatory and chemokinetic properties

SEQ ID : 12

Description: Deletion of 5 amino acids between the positions 65-69 of the original protein. Replacement of the amino acid at the position 70 of the original protein by an alternative amino acid. Missing part of strand.

Accession: TSP1_HUMAN

Name: Thrombospondin adhesive glycoprotein

Function: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type v collagen

SEQ ID : 13

35

Description: Truncated exact 1-722 (731aa long compared to 1170aa), last 9 amino acids are different. Missing 7 X TSP TYPE-3 REPEATS CA-BINDING

- 41 -

domain C-TERMINAL, missing CELL ATTACHMENT SITE, missing 1 out of 4 glycosylation sites. Has all other components including signal peptide

Accession: TSP1_HUMAN

5 **Name:** Thrombospondin adhesive glycoprotein

Function: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type v collagen

10 **SEQ ID : 14**

Description: Truncated exact 1-548 (555aa long compared to 1170) last 7aa different. Missing 3 X EGF-TYPE REPEATS, missing 7 X TSP TYPE-3 REPEATS Ca-BINDING domain C-TERMINAL missing CELL
15 ATTACHMENT SITE, missing all diSulfide bonds, missing 2 out of 4 glycosylation sites. Has all other domains (including signal peptide).

Accession: TSP1_HUMAN

Name: Thrombospondin adhesive glycoprotein

20 **Function:** Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type v collagen

SEQ ID : 15

25 **Description:** Truncated exact 1-490 (546aa long compared to 1170) last 56 amino acids are different. Missing 1 out of 3 X TSP TYPE-1 REPEATS (CS-LIKE), Missing 3 X EGF-TYPE REPEATS, missing 7 X TSP TYPE-3 REPEATS CA-BINDING domain C-TERMINAL missing CELL
30 ATTACHMENT SITE, missing all diSulfide bonds, missing 2 out of 4 glycosylations. Has all other domains (including signal peptide).

Accession: TSP1_HUMAN

Name: Thrombospondin adhesive glycoprotein

35 **Function:** Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin and type v collagen

- 42 -

SEQ ID : 16

Description: Truncated: exact 1-431aa (459aa long compared to 1170) last 28
5 amino acids are different. Missing 2 out of 3 X TSP TYPE-1 REPEATS
(CS-LIKE), Missing 3 X EGF-TYPE REPEATS, missing 7 X TSP TYPE-3
REPEATS CA-BINDING domain C-TERMINAL missing CELL
ATTACHMENT SITE, missing all diSulfide bonds, missing 2 out of 4
glycosylations. Has all other domains (including signal peptide).

10

Accession: TYPH_HUMAN

Name: PLATELET-DERIVED ENDOTHELIAL CELL GROWTH
FACTOR

Function: May have a role in maintaining the integrity of the blood
15 vessels. Has growth promoting activity on endothelial cells,
angiogenic activity *in vivo* and chemotactic activity on
endothelial cells *in vitro*.

20

CATALYSES THE REVERSIBLE PHOSPHOROLYSIS
OF THYMIDINE. THE PRODUCED MOLECULES ARE
THEN UTILIZED AS CARBON AND ENERGY
SOURCES OR IN THE RESCUE OF PYRIMIDINE
BASES FOR NUCLEOTIDE SYNTHESIS.

25

SIMILARITY: BELONGS TO THYMIDINE/
PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASES
FAMILY.

SEQ ID : 17

Description: Deletion of 119 amino acids between the positions 333-452 of
30 the original protein. The resulting new variant is missing the 3rd repeat of the
original protein.

Accession: TYPH_HUMAN

Name: PLATELET-DERIVED ENDOTHELIAL CELL GROWTH
35 FACTOR

- 43 -

Function: May have a role in maintaining the integrity of the vessels. Has growth promoting activity on endothelial cells, angiogenic activity in vivo and chemotactic activity on endothelial cells *in vitro*.

5 CATALYSES THE REVERSIBLE PHOSPHOROLYSIS OF THYMIDINE. THE PRODUCED MOLECULES ARE THEN UTILIZED AS CARBON AND ENERGY SOURCES OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.

10 SIMILARITY: BELONGS TO THYMIDINE/PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASES FAMILY.

SEQ ID : 18

15

Description: Replacement of 48 amino acids between the positions 216-264 of the original protein by alternative 9 amino acids.

Accession: TYPH_HUMAN

20

Name: PLATELET-DERIVED ENDOTHELIAL CELL GROWTH FACTOR

Function: May have a role in maintaining the integrity of the vessels. Has growth promoting activity on endothelial cells, angiogenic activity in vivo and chemotactic activity on endothelial cells *in vitro*.

25

CATALYSES THE REVERSIBLE PHOSPHOROLYSIS OF THYMIDINE. THE PRODUCED MOLECULES ARE THEN UTILIZED AS CARBON AND ENERGY SOURCES OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.

30

SIMILARITY: BELONGS TO THYMIDINE/PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASES FAMILY.

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SEQ ID : 19

Description: Deletion of 119 amino acids between the positions 333-452, missing 3rd repeat of the original protein. Replacement of 48 amino acids
5 between the positions 216-264 of the original protein by alternative 9 amino acids.

Accession: IC1_HUMAN

Name: PLASMA PROTEASE C1 INHIBITOR

10 **Function:** Activation of the c1 complex is under control of the c1-. Inhibitor. IT FORMS A PROTEOLYTICALLY INACTIVE STOICHIOMETRIC COMPLEX WITH THE C1R OR C1S PROTEASES. MAY PLAY A POTENTIALLY CRUCIAL
15 ROLE IN REGULATING IMPORTANT PHYSIOLOGICAL PATHWAYS INCLUDING COMPLEMENT ACTIVATION, BLOOD COAGULATION, FIBRINOLYSIS AND THE GENERATION OF KININS.
PTM: HIGHLY GLYCOSYLATED (49%).
20 SIMILARITY: BELONGS TO THE SERPIN FAMILY.

SEQ ID NO : 20

Description: Deletion of 19 amino acids between the positions 29-48 of the
25 original protein. Missing 1 glycosylation out of 14.

Accession: PTI6_HUMAN

Name: PLACENTAL THROMBIN INHIBITOR

Function: Cytoplasmic antiproteinase.
30 SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.

SEQ ID : 21

35 **Description:** Deletion of 261 N-terminal amino acids of the original protein (the first possible Met is at the position 261). The new variant has 116 amino

- 45 -

acids compared to 376 in the original protein (exact 261-376), including the active site.

Accession: PTI6_HUMAN

Name: PLACENTAL THROMBIN INHIBITOR

5 **Function:** Cytoplasmic antiproteinase
SIMILARITY: BELONGS TO THE SERPIN FAMILY.
OV-SERPIN SUBFAMILY.

SEQ ID : 22

10

Description: Deletion of 57 amino acids between the positions 267-325 of the original protein. The resulting new variant contains the active site.

Accession: PTI6_HUMAN

Name: PLACENTAL THROMBIN INHIBITOR

15 **Function:** Cytoplasmic antiproteinase

SEQ ID : 23

20 **Description:** Deletion of 189 amino acids between the positions 89-278 of the original protein. The resulting new variant contains the active site.

Accession: PTI6_HUMAN

Name: PLACENTAL THROMBIN INHIBITOR

Function: Cytoplasmic antiproteinase

25

SEQ ID : 24

30 **Description:** Replacement of 376 C-terminal amino acids of the original protein by alternative 5 amino acids. The resulting new variant doesn't contain the active site.

Accession: IAP2_HUMAN

Name: INHIBITOR OF APOPTOSIS PROTEIN 2

35 **Function:** Apoptotic suppressor. The BIR motifs region interacts with TNF receptor associated factors 1 and 2 (traf1 and traf2) to form an heteromeric complex, which is then recruited to the tumor necrosis factor receptor 2 (TNFR2).

- 46 -

SEQ ID : 25

Description: Truncated: 305 amino acids compared to 618 aa(protein 2). The
5 new variant contains exact positions 1-299, last 6 amino acids are different. Two
SNIPs in positions 235 and 241 of the original protein. The new variant is
missing Zn Finger and half of 3rd BIR repeat.

Accession: SET_HUMAN
10 **Name:** PHOSPHATASE 2A INHIBITOR I2PP2A
Function: May be involved in the generation of intracellular signaling
events that lead to regulation of transcriptional activity after
binding of a ligand to HLA class II molecules. Potent
inhibitor of protein phosphatase 2a.

15

SEQ ID : 26

Description: Extra 83 amino acids in the N-terminus of the protein. The
added sequence has predicted potential transmembrane domain (probable signal
20 peptide?)

Accession: SET_HUMAN
Name: PHOSPHATASE 2A INHIBITOR I2PP2A
Function: May be involved in the generation of intracellular signaling
25 events that lead to regulation of transcriptional activity after
binding of a ligand to HLA class II molecules. Potent
inhibitor of protein phosphatase 2a.

SEQ ID : 27

30

Description: Replacement of 24 C-terminal amino acids of the original
protein by alternative 8 amino acids. Missing part of ASP/GLU-RICH and
BREAKPOINT FOR TRANSLOCATION TO FORM SET-CAN
ONCOGENE.

35

Accession: CDNC_HUMAN
Name: CYCLIN-DEPENDENT KINASE INHIBITOR 1C

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Function: POTENT TIGHT-BINDING INHIBITOR OF SEVERAL
G1 CYCLIN/CDK COMPLEXES (CYCLIN E-CDK2,
CYCLIN D2-CDK4, AND CYCLIN A-CDK2) AND, TO
LESSER EXTENT, OF THE MITOTIC CYCLIN B-CDC2.
NEGATIVE REGULATOR OF CELL PROLIFERATION.
MAY PLAY A ROLE IN MAINTENANCE OF THE
NONPROLIFERATIVE STATE THROUGHOUT LIFE.
SUBCELLULAR LOCATION: NUCLEAR (BY
SIMILARITY).
DISEASE: CDKN1C MUTATIONS ARE INVOLVED IN
TUMOR FORMATION.

SEQ ID : 28

Description: Deletion of 178 amino acids at the positions 97-275 of the
original protein. Insertion of 121 amino acids at the N-terminus. The resulting
new variant is missing PAPA repeats.

Accession: F13B_MOUSE

Name: COAGULATION FACTOR XIII B CHAIN

Function: The B chain of factor XIII is not catalytically active, but is
thought to stabilize the a subunits and regulate the rate of
transglutaminase formation by thrombin

25 SEQ ID : 29**Description**

Deletion of 87 C-terminal amino acids of the original protein. SNIP at position
236 (L->V). The resulting new variant is missing the last shushi repeat.

Accession: EGF_MOUSE

Name: PRO-EPIDERMAL GROWTH FACTOR

Function: Stimulates the growth of various epidermal and epithelial
tissues.

35 SEQ ID : 30

- 48 -

Description: Deletion of 641 amino acids between the positions 67-708 of the original protein. Missing 4 EGF-like domains, 2 glycosylations, 9 diSulfide bonds.

5 **Accession:** EGF_MOUSE
Name: PRO-EPIDERMAL GROWTH FACTOR
Function: Stimulates the growth of various epidermal and epithelial Tissues

- 49 -

SEQ ID : 31

Description: Deletion of 641 amino acids between the positions 67-708, and deletion of 45 amino acids between the positions 1020-1065 of the original protein. Missing 4 EGF-like domains, 2 glycosylations, 9 diSulfide bonds. Missing transmembrane domain.

Accession: EGF_MOUSE
Name: PRO-EPIDERMAL GROWTH FACTOR
Function: Stimulates the growth of various epidermal and epithelial tissues

SEQ ID : 32

Description: Deletion of 641 amino acids between the positions 67-708 of the original protein. Missing 4 EGF-like domains, 2 glycosylations, 9 diSulfide bonds. Replacement of 419 C-terminal amino acids by 5 amino acids.

Accession: EGF_MOUSE
Name: PRO-EPIDERMAL GROWTH FACTOR
Function: Stimulates the growth of various epidermal and epithelial Tissues

SEQ ID : 33

Description: Deletion of 841 amino acids between the positions 18-859 of the original protein. Missing 5 EGF-like domains and 2 glycosylation sites.

Accession: EGF_MOUSE
Name: PRO-EPIDERMAL GROWTH FACTOR
Function: Stimulates the growth of various epidermal and epithelial Tissues

- 50 -

SEQ ID : 34

Description: Deletion of 774 amino acids between the positions 5-779 of the original protein. Missing signal peptide, 5 EGF-like domains, and 2 glycosylation sites.

Accession: P53_MOUSE
Name: CELLULAR TUMOR ANTIGEN P53
Function: Acts as a tumor suppressor in many tumor types. Induces growth arrest or apoptosis depending on the physiological circumstances or cell type, but both activities are involved in tumor suppression.

SEQ ID : 35

Description: Deletion of 336 N-terminal amino acids of the original protein. Missing ASP/GLU-RICH (ACIDIC), missing hydrophobic domain, missing NUCLEAR LOCALIZATION SIGNAL, missing 1 out of 2 PHOSPHORYLATION sites.

Accession: NME3_HUMAN
Name: GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3
Function: NMDA receptor subtype of glutamate-gated ion channels possesses high calcium permeability and voltage-dependent sensitivity to magnesium and is mediated by glycine.

SEQ ID : 36

Description: Deletion of 381 N-terminal amino acids of the original protein. Missing 2 out of 4 glycosylation sites.

Accession: TRFE_HUMAN
Name: SEROTRANSFERRIN
Function: Iron binding transport proteins

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SEQ ID : 37

Description: Deletion of 34 amino acids between the positions 654-689 of the original protein. Loss of disulfide bond.

5

Accession: TRFE_HUMAN
Name: SEROTRANSFERRIN
Function: Iron binding transport proteins

10 **SEQ ID : 38**

Description: Deletion of 52 amino acids between the positions 447-499 of the original protein. Loss of disulfide bond.

15 **Accession:** BAA23795
Name: Brain ryanodine receptor

SEQ ID : 39

20

Description: Replacement of 83 C-terminal amino acids from probable cytoplasmic domain of the original protein by alternative 4 amino acids. Resulting in truncated new variant: 4787 compared to 4866, exact 1-4783 with last 4 amino acids different.

25

Accession: VIPS_HUMAN
Name: VASOACTIVE INTESTINAL POLYPEPTIDE
RECEPTOR 2

30

Function: This is a receptor for VIP as well as PACAP-38 and -27, the activity of this receptor is mediated by G proteins which activate adenylyl cyclase. Can be coupled to phospholipase C.

SEQ ID : 40

35 **Description:** Replacement of 64 C-terminal amino acids of the original protein by alternative 7 amino acids. The resulting new variant is missing the last transmembrane and the cytoplasmic domains.

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Accession: PACR_HUMAN
Name: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE RECEPTOR

Function: This is a receptor for PACAP-27 and PACAP-38. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase. May regulate the release of adrenocorticotropin, luteinizing hormone, growth hormone, prolactin, epinephrine.

10 **SEQ ID : 41**

Description: Deletion of 22 amino acids between the positions 88-110 of the original protein. The deletion is in extracellular loop.

15 **Accession:** NRP_HUMAN
Name: NEUROPILIN VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165 RECEPTOR

Function: Calcium-independent cell adhesion molecule that function during the formation of certain neuronal circuits. Binds to semaphorin III and to the VEGF165 isoform of VEGF

20 **SEQ ID : 42**

Description: Deletion of 540 C-terminal amino acids of the original protein, resulting in truncated new variant (383 compared to 923 amino acids).

The new variant is missing part of the extracellular domain, the cytoplasmic and the transmembrane domains.

Accession: NRP_HUMAN
30 **Name:** NEUROPILIN VASCULAR ENDOTHELIAL CELL GROWTH FACTOR 165 RECEPTOR

Function: Calcium-independent cell adhesion molecule that during the formation of certain neuronal circuits. Binds to semaphorin III and to the VEGF165 isoform of VEGF

35

- 53 -

R2_NV43

Description: Replacement of 595 C-terminal amino acids of the original protein by alternative 11 amino acids. The resulting new variant is truncated (339
5 compared to 923 amino acids, exact 1-328 with last 11 amino acids different), and is missing part of the extracellular domain, the cytoplasmic and the transmembrane domains.

Accession: gi|1899200

10 **Name:** N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2A

Function: NMDA RECEPTOR SUBTYPE OF GLUTAMATE-
GATED ION CHANNELS POSSESSES HIGH CALCIUM
PERMEABILITY AND VOLTAGE-DEPENDENT
15 SENSITIVITY TO MAGNESIUM AND IS MEDIATED
BY GLYCINE.

SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT
AND A ZETA SUBUNIT.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
PROTEIN.

20 **SIMILARITY:** BELONGS TO THE LIGAND-GATED
IONIC CHANNELS FAMILY.

SEQ ID : 44:

25 **Description:** Deletion of 114 amino acids between the positions
1257-1372 of the original protein.

Accession: VIPS_HUMAN

Name: VASOACTIVE INTESTINAL POLYPEPTIDE
30 RECEPTOR 2

Function: THIS IS A RECEPTOR FOR VIP AS WELL AS
PACAP-38 AND -27, THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH
ACTIVATE ADENYLYL CYCLASE. CAN BE
35 COUPLED TO PHOSPHOLIPASE C.

SUBCELLULAR LOCATION: INTEGRAL
MEMBRANE PROTEIN.

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SIMILARITY: BELONGS TO FAMILY 2 OF
G-PROTEIN COUPLED RECEPTORS.

SEQ ID : 45:

5

Description: Replacement of 56 C-terminal amino acids from the cytoplasmic domain of the original protein by alternative 73 amino acids.

10 **SEQ ID : 46**

Description: Replacement of 56 C-terminal amino acids from the cytoplasmic domain of the original protein by alternative 70 amino acids.

15

Accession: IG1R_HUMAN

Name: INSULIN-LIKE GROWTH FACTOR I RECEPTOR
PRECURSOR

20

Function: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH
FACTOR I (IGF I) WITH A HIGH AFFINITY AND IGF II
WITH A LOWER AFFINITY. IT HAS A
TYROSINE-PROTEIN KINASE ACTIVITY.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
= ADP + PROTEIN TYROSINE PHOSPHATE.

25

SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA
CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA
CHAINS

CONTRIBUTE TO THE FORMATION OF THE LIGAND-
BINDING DOMAIN, WHILE THE BETA CHAIN
CARRIES THE KINASE DOMAIN.

30

SUBCELLULAR LOCATION: TYPE I MEMBRANE
PROTEIN.

SIMILARITY: BELONGS TO THE INSULIN RECEPTOR
FAMILY OF TYROSINE- PROTEIN KINASES.

35

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE
III-LIKE DOMAINS.

- 55 -

SEQ ID : 47

Description: Deletion of 22 amino acids between the positions 1268-1291 of the original protein. The deleted fragment is part of the cytoplasmic domain of
5 INSULIN-LIKE GROWTH FACTOR I RECEPTOR, BETA-CHAIN.

Accession: NRP_HUMAN

Name: NEUROPILIN

10 **Function:** CALCIUM-INDEPENDENT CELL ADHESION
MOLECULE THAT FUNCTION DURING THE
FORMATION OF CERTAIN NEURONAL CIRCUITS.
BINDS TO SEMAPHORIN III AND TO THE VEGF165
ISOFORM OF VEGF.
15 SUBCELLULAR LOCATION: TYPE I MEMBRANE
PROTEIN.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.

20

SEQ ID : 48

Description: Replacement of 282 C-terminal amino acids of the original protein, including the transmembrane domain and the MAM domain, by
25 alternative 3 amino acids.

SEQ ID : 49

Description: Deletion of 83 amino acids between the positions 538-622 of
30 the original protein. The deleted region includes part of the F5/8 TYPE C 2 domain and part of the MAM domain.

SEQ ID : 50

35 **Description:** Deletion of 385 C-terminal amino acids of the original protein, including the transmembrane domain and the MAM domain.

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Accession: FGR3_HUMAN

Name: FIBROBLAST GROWTH FACTOR RECEPTOR 3

Function: SUBCELLULAR LOCATION: TYPE I MEMBRANE
PROTEIN.

5

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15

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25

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35

DISEASE: DEFECTS IN FGFR3 ARE THE CAUSE OF THE AUTOSOMAL DOMINANT DISEASE ACHONDROPLASIA (ACH); THE MOST FREQUENT FORM OF SHORT-LIMB DWARFISM. ACH IS CHARACTERIZED BY A LONG, NARROW TRUNK, SHORT EXTREMITIES, PARTICULARLY IN THE PROXIMAL (RHIZOMELIC) SEGMENTS, A LARGE HEAD WITH FRONTAL BOSSING, HYPOPLASIA OF THE MIDFACE AND A TRIDENT CONFIGURATION OF THE HANDS.

DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF CROUZON SYNDROME, ALSO CALLED CRANIOFACIAL DYSOSTOSIS TYPE I (CFD1). CHARACTERIZED BY CRANIOSYNOSTOSIS (PREMATURE FUSION OF THE SKULL SUTURES), HYPERTELORISM, EXOPHTHALMOS AND EXTERNAL STRABISMUS, PARROT-BEAKED NOSE, SHORT UPPER LIP, HYPOPLASTIC MAXILLA, AND A RELATIVE MANDIBULAR PROGNATHISM.

DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF THANATOPHORIC DYSPLASIA (TD) (ALSO KNOWN AS THANATOPHORIC DWARFISM), THE MOST COMMON NEONATAL LETHAL SKELETAL DYSPLASIA, AFFECTED INDIVIDUALS DISPLAY FEATURES SIMILAR TO THOSE SEEN IN HOMOZYGOUS ACHONDROPLASIA. IT CAUSES SEVERE SHORTENING OF THE LIMBS WITH MACROCEPHALY, NARROW THORAX AND SHORT RIBS. IN THE MOST COMMON SUBTYPE (TD1), FEMUR ARE CURVED, WHILE IN TD2, STRAIGHT FEMURS ARE ASSOCIATED WITH CLOVERLEAF SKULL.

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DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF CRANIOSYNOSTOSIS ADELAIDE TYPE (CRS3), A FORM OF CORONAL SYNOSTOSIS (CS) CHARACTERIZED BY CRANIOSYNOSTOSIS, MIDFACE HYPOPLASIA, DOWNSLANDING PALPEBRAL FISSURES, PTOSIS, HIGHLY ARCHED PALATE, MID-TO-MODERATE SENSORINEURAL HEARING LOSS, NORMAL STATURE, BRADYDACTYLY, BROAD BIG TOES. RADIOLOGICALY HANDS AND FEET SHOW THIMBLE-LIKE MIDDLE PHALANGES, CONED EPIPHYSES, AND CARPAL AND TARSAL FUSIONS.

DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF THE AUTOSOMAL DOMINANT DISEASE HYPOCHONDROPLASIA CHARACTERIZED BY DISPROPORTIONATE SHORT STATURE. IT RESEMBLE ACHONDROPLASIA, BUT WITH A LESS SEVERE PHENOTYPE.

SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR FAMILY.

SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE DOMAINS.

SEQ ID : 51

Description: Replacement of 496 C-terminal amino acids of the original protein by alternative 79 amino acids.. The deleted region includes the C-terminal part of the extracellular domain, the transmembrane domain, the cytoplasmic domain, the protein kinase domain and the two ATP binding domains.

EGF MOUSE

EPIDERMAL GROWTH FACTOR

FUNCTION: THE GROWTH FACTOR STIMULATES THE GROWTH OF VARIOUS EPIDERMAL AND EPITHELIAL TISSUES IN VIVO AND IN VITRO AND OF SOME FIBROBLASTS IN CELL CULTURE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

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SIMILARITY: CONTAINS 8 COMPLETE AND ONE INCOMPLETE EGF-LIKE DOMAINS.

SEQ ID NO : 52

5

Deletion of 144 amino acids between the positions 1020-1165, including the transmembrane domain and part of the cytoplasmic domain of the original protein.

10 **SEQ ID NO : 53**

Replacement of 418 C-terminal amino acids of the original protein by alternative 5 amino acids. The deleted region includes the EGF active chain, 4 out of 9 EGF-like domains within the extracellular region of the protein, the
15 transmembrane and the cytoplasmic regions.

SEQ ID NO : 54

Deletion of 641 amino acids between the positions 66-707 of the original protein.
20 The deleted region is in the extracellular part of the protein and it includes 4 out of 9 EGF-like domains. NV-20 contains the original signal peptide, part of the extracellular domain, the epidermal growth factor chain (located between the positions 977-1029 of the original protein), and the original transmembrane and the cytoplasmic domains.

25

SEQ ID NO : 55

Deletion of 842 amino acids between the positions 17-859 of the original protein
30 (including replacement of the amino acid in the position 859 by an alternative one). The deleted region is in the extracellular part of the protein and it includes 5 out of 9 EGF-like domains. NV-20 contains the original signal peptide, part of the extracellular domain, the epidermal growth factor chain (located between the positions 977-1029 of the original protein), and the original transmembrane and
35 the cytoplasmic domains.

ACE_MOUSE

40

ANGIOTENSIN-CONVERTING ENZYME

- 59 -

FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY
RELEASE OF THE TERMINAL HIS-LEU, THIS RESULTS IN AN
5 INCREASE OF THE VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CATALYTIC ACTIVITY: RELEASE OF A C-TERMINAL DIPEPTIDE,
OLIGOPEPTIDE-|-XAA-XBB, WHEN XAA IS NOT PRO, AND XBB IS
NEITHER ASP NOR GLU. CONVERTS ANGIOTENSIN I TO
ANGIOTENSIN II.

10 COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: THE TESTICULAR ANGIOTENSIN-
CONVERTING ENZYME IS TRANSCRIBED FROM THE SAME GENE AS
THE SOMATIC ISOFORM, PROBABLY FROM AN ALTERNATIVE START
15 SITE.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2 (ZINC
METALLOPROTEASE).

20 SEQ ID NO : 56

Replacement of 77 C-terminal amino acids of the original protein, including the
entire transmembrane and cytoplasmic domains, by alternative 14 amino acids.

25 ESRI_MOUSE

ESTROGEN RECEPTOR

30 FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE
INVOLVED IN THE REGULATION OF EUKARYOTIC GENE
EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND
DIFFERENTIATION IN TARGET TISSUES.

SUBUNIT: HOMODIMER.

35 SUBCELLULAR LOCATION: NUCLEAR.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING
N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A
C-TERMINAL STEROID-BINDING DOMAIN.

40 MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE
RECEPTORS ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH
NUCLEAR COMPONENTS; HORMONE BINDING GREATLY INCREASES
RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS
TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM OF
TRANSCRIPTIONAL START SITES.

- 60 -

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
FAMILY. NR3 SUBFAMILY.

SEQ ID : 57

5

Replacement of 229 C-terminal amino acids of the original protein, including part of the steroid-binding domain, by an alternative 12 amino acids.

10

FA7_MOUSE**COAGULATION FACTOR VII PRECURSOR**

15 FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM.
FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA,
FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS.
IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR
VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED
20 PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM
(BY SIMILARITY).

CATALYTIC ACTIVITY: HYDROLYSES ONE ARG-|-ILE BOND IN
FACTOR X TO FORM FACTOR XA.

25 SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN
LINKED BY A DISULFIDE BOND (BY SIMILARITY).

TISSUE SPECIFICITY: PLASMA.

PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION
OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED
30 PROTEIN TO BIND CALCIUM (BY SIMILARITY).

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
THE TRYPSIN FAMILY.

35 SEQ ID : 58

Deletion of 101 amino acids, between the positions 119-220 of the original
protein. The deleted region contains 74 amino acids from the C-terminal end of
the factor VII light chain, and 26 amino acids from the N-terminal end of the
40 factor VII heavy catalytic chain. The deleted region includes EGF-like 2 domain
and the cleavage site (by factor XA, factor XIIA, factor IXA, or thrombin) of

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the original protein.

CAL0_MOUSE

5

CALCITONIN PRECURSOR

FUNCTION: CAUSES A RAPID BUT SHORT-LIVED DROP IN THE LEVEL
OF CALCIUM AND PHOSPHATE IN BLOOD BY PROMOTING THE
10 INCORPORATION OF THOSE IONS IN THE BONES.

ALTERNATIVE PRODUCTS: THE CALCITONIN PRECURSOR AND THE
CALCITONIN RELATED PEPTIDE PRECURSOR ARE OBTAINED BY
TISSUE-SPECIFIC SPLICING OF THE SAME GENE.

SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.

15

SEQ ID NO : 59

Deletion of 33 amino acids, spanning the positions 18-50, between the signal and
the calcitonin peptide in the original precursor protein.

20

gi 2826776

VESICULAR INHIBITORY AMINO ACID TRANSPORTER

25

function="uptake of GABA and glycine into synaptic vesicles"

SEQ ID NO : 60

30

Replacement of the last 7 C-terminal amino acids of the original protein by
alternative 11 amino acids.

35

PTI6_HUMAN

PLACENTAL THROMBIN INHIBITOR

40

CYTOPLASMIC ANTIPROTEINASE, PROTEASE INHIBITOR 6.
SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN
SUBFAMILY.

- 62 -

SEQ ID NO : 61

Replacement of the last 4 C-terminal amino acids of the original protein by alternative 28 amino acids.

5

SEQ ID NO : 62

Replacement of the last 16 C-terminal amino acids of the original protein by alternative 12 amino acids.

10

RIN1_HUMAN

15

RAS INTERACTION/INTERFERENCE PROTEIN 1
(RAS INHIBITOR JC99)
(FRAGMENT)

SEQ ID NO : 63

20

Replacement of 158 last C-terminal amino acids of the original protein by alternative 71 amino acids with probable transmembrane region.

25

CDNC_HUMAN**CYCLIN-DEPENDENT KINASE INHIBITOR 1C P57**

30

FUNCTION: POTENT TIGHT-BINDING INHIBITOR OF SEVERAL G1 CYCLIN/CDK COMPLEXES (CYCLIN E-CDK2, CYCLIN D2-CDK4, AND CYCLIN A-CDK2) AND, TO LESSER EXTENT, OF THE MITOTIC CYCLIN B-CDC2. NEGATIVE REGULATOR OF CELL PROLIFERATION. MAY PLAY A ROLE IN MAINTENANCE OF THE NONPROLIFERATIVE STATE THROUGHOUT LIFE.

35

SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DISEASE: CDKN1C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.

40

SEQ ID NO : 64

Addition of 121 amino acids at the N-terminus of the protein.

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CDN2_HUMAN

5 **CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I)**
 (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1)

10 FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS
 ITS ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A
 NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL
 CELLS.

 SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.

15 DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR
 FORMATION IN A WIDE RANGE OF TISSUES.

 SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF
 CYCLIN-DEPENDENT KINASE INHIBITORS.

 SIMILARITY: CONTAINS 4 ANK REPEATS.

20

SEQ ID NO : 65

 Replacement of 5 amino acids at the positions 18, 24, 27, 30, 37 of the original
 protein by alternative amino acids. Replacement of last 4 C-terminal amino acids
25 of the original protein by alternative 20 amino acids.

CDN5_HUMAN

30 **CYCLIN-DEPENDENT KINASE 4 INHIBITOR B**
 (MULTIPLE TUMOR SUPPRESSOR 2)

35 FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT
 INHIBITOR. POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL
 CYCLE ARREST.

 SUBUNIT: HETERODIMER OF P14 WITH CDK4.

 DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR
 FORMATION.

40 SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF
 CYCLIN-DEPENDENT KINASE INHIBITORS.

 SIMILARITY: CONTAINS 2 ANK REPEATS.

- 64 -

SEQ ID NO : 66

Replacement of the last 6 C-terminal amino acids of the original protein by alternative 52 amino acids.

5

HEP2_HUMAN

HEPARIN COFACTOR II PRECURSOR
PROTEASE INHIBITOR LEUSERPIN 2

10

FUNCTION: THROMBIN INHIBITOR ACTIVATED BY THE GLYCOSAMINOGLYCANS, HEPARIN OR DERMATAN SULFATE. IN THE PRESENCE OF THE LATTER, HC-II BECOMES THE PREDOMINANT THROMBIN INHIBITOR IN PLACE OF ANTITHROMBIN III (AT). ALSO INHIBITS CHYMOTRYPSIN, BUT IN A GLYCOSAMINOGLYCAN-INDEPENDENT MANNER.

15

FUNCTION: PEPTIDES AT THE N-TERMINAL OF HC-II HAVE CHEMOTACTIC ACTIVITY FOR BOTH MONOCYTES AND NEUTROPHILS.

20

TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LIVER.

DOMAIN: THE N-TERMINAL ACIDIC REPEAT REGION MEDIATES, IN PART, THE

GLYCOSAMINOGLYCAN-ACCELERATED THROMBIN INHIBITION.

DISEASE: DEFECTS IN HCF2 ARE ASSOCIATED WITH THROMBOSIS (THROMBOPHILIA).

25

SIMILARITY: BELONGS TO THE SERPIN FAMILY.

SEQ ID NO : 67

30 Deletion of 150 amino acids, between the positions 334-485, of the original protein. The deleted region includes the reactive bond (the active site) of the original protein. NV-33 does contain the chemotactic activity domain, the glycosaminoglycan-binding site and the hirudin-like 2 x 11 AA approximate repeats, Asp/Glu rich.

35

TFP2_HUMAN

TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR

40

FUNCTION: SEEMS TO INHIBIT TRYPSIN, FACTOR VII(A)/TISSUE FACTOR, WEAKLY FACTOR XA. HAS NO EFFECT ON THROMBIN.

- 65 -

DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
SIMILARITY: BELONGS TO THE BPTI/KUNITZ FAMILY OF
INHIBITORS. HIGHLY SIMILAR TO TPFI.

5 **SEQ ID NO : 68**

Replacement of 36 C-terminal amino acids of the original protein by alternative
12 amino acids. The deleted region includes part of the BPTI/KUNITZ inhibitor
domain-3 and the poly-Lysine domain of the original protein.

10

SEQ ID NO : 69

Deletion of 25 amino acids, between the positions 153-178 of the original
15 protein, and replacement of the amino acid at the position 179 by alternative one.
The deleted region includes the active site and part of the BPTI/KUNITZ
inhibitor domain-3.

20

TFPI_HUMAN

TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR (TFPI)

25 **SEQ ID NO : 70**

Replacement of 95 C-terminal amino acids of the original protein, containing the
entire BPTI/KUNITZ inhibitor-3 domain, by alternative 16 amino acids.

30

Example II: Variant nucleic acid sequence

The nucleic acid sequences of the invention include nucleic acid
sequences which encode variant product and fragments and analogs thereof. The
nucleic acid sequences may alternatively be sequences complementary to the
35 above coding sequence, or to a region of said coding sequence. The length of the
complementary sequence is sufficient to avoid the expression of the coding
sequence. The nucleic acid sequences may be in the form of RNA or in the form
of DNA, and include messenger RNA, synthetic RNA and DNA, cDNA, and
genomic DNA. The DNA may be double-stranded or single-stranded, and if

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single-stranded may be the coding strand or the non-coding (anti-sense, complementary) strand. The nucleic acid sequences may also both include dNTPs, rNTPs as well as non naturally occurring sequences. The sequence may also be a part of a hybrid between an amino acid sequence and a nucleic acid
5 sequence.

In a general embodiment, the nucleic acid sequence has at least 90%, identity with any one of the sequence identified as SEQ ID NO: 1 to SEQ ID NO: 174 provided that this sequence is not completely identical with that of the original sequence.

10 The nucleic acid sequences may include the coding sequence by itself. By another alternative the coding region may be in combination with additional coding sequences, such as those coding for fusion protein or signal peptides, in combination with non-coding sequences, such as introns and control elements, promoter and terminator elements or 5' and/or 3' untranslated regions, effective
15 for expression of the coding sequence in a suitable host, and/or in a vector or host environment in which the variant nucleic acid sequence is introduced as a heterologous sequence.

The nucleic acid sequences of the present invention may also have the product coding sequence fused in-frame to a marker sequence which allows for
20 purification of the variant product. The marker sequence may be, for example, a hexahistidine tag to provide for purification of the mature polypeptide fused to the marker in the case of a bacterial host, or, the marker sequence may be a hemagglutinin (HA) tag when a mammalian host, e.g. COS-7 cells, is used. The HA tag corresponds to an epitope derived from the influenza hemagglutinin
25 protein (Wilson, I., *et al. Cell* 37:767 (1984)).

Also included in the scope of the invention are fragments as defined above also referred to herein as oligonucleotides, typically having at least 20 bases, preferably 20-30 bases corresponding to a region of the coding-sequence nucleic acid sequence. The fragments may be used as probes, primers, and when

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complementary also as antisense agents, and the like, according to known methods.

As indicated above, the nucleic acid sequence may be substantially a depicted in any one of SEQ ID NO: 1 to SEQ ID NO: 87 or fragments thereof or
5 sequences having at least 90% identity to the above sequence as explained above. Alternatively, due to the degenerative nature of the genetic code, the sequence may be a sequence coding for any one of the amino acid sequence of SEQ ID NO: 88 to SEQ ID NO: 174, or fragments or analogs of said amino acid sequence.

10

A. Preparation of nucleic acid sequences

The nucleic acid sequences may be obtained by screening cDNA libraries using oligonucleotide probes which can hybridize to or PCR-amplify nucleic acid sequences which encode the variant products disclosed above. cDNA libraries
15 prepared from a variety of tissues are commercially available and procedures for screening and isolating cDNA clones are well-known to those of skill in the art. Such techniques are described in, for example, Sambrook *et al.* (1989) Molecular Cloning: A Laboratory Manual (2nd Edition), Cold Spring Harbor Press, Plainview, N.Y. and Ausubel FM *et al.* (1989) Current Protocols in Molecular
20 Biology, John Wiley & Sons, New York, N.Y.

The nucleic acid sequences may be extended to obtain upstream and downstream sequences such as promoters, regulatory elements, and 5' and 3' untranslated regions (UTRs). Extension of the available transcript sequence may be performed by numerous methods known to those of skill in the art, such as
25 PCR or primer extension (Sambrook *et al.*, *supra*), or by the RACE method using, for example, the Marathon RACE kit (Clontech, Cat. # K1802-1).

Alternatively, the technique of "restriction-site" PCR (Gobinda *et al.* *PCR Methods Applic.* 2:318-22, (1993)), which uses universal primers to retrieve flanking sequence adjacent a known locus, may be employed. First, genomic
30 DNA is amplified in the presence of primer to a linker sequence and a primer

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specific to the known region. The amplified sequences are subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

5 Inverse PCR can be used to amplify or extend sequences using divergent primers based on a known region (Triglia, T. *et al.*, *Nucleic Acids Res.* 16:8186, (1988)). The primers may be designed using OLIGO(R) 4.06 Primer Analysis Software (1992; National Biosciences Inc, Plymouth, Minn.), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of
10 50% or more, and to anneal to the target sequence at temperatures about 68-72°C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Capture PCR (Lagerstrom, M. *et al.*, *PCR Methods Applic.* 1:111-19,
15 (1991)) is a method for PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA. Capture PCR also requires multiple restriction enzyme digestions and ligations to place an engineered double-stranded sequence into a flanking part of the DNA molecule before PCR.

20 Another method which may be used to retrieve flanking sequences is that of Parker, J.D., *et al.*, *Nucleic Acids Res.*, 19:3055-60, (1991)). Additionally, one can use PCR, nested primers and PromoterFinder™ libraries to "walk in" genomic DNA (PromoterFinder™; Clontech, Palo Alto, CA). This process avoids the need to screen libraries and is useful in finding intron/exon junctions. Preferred
25 libraries for screening for full length cDNAs are ones that have been size-selected to include larger cDNAs. Also, random primed libraries are preferred in that they will contain more sequences which contain the 5' and upstream regions of genes.

A randomly primed library may be particularly useful if an oligo d(T) library does not yield a full-length cDNA. Genomic libraries are useful for
30 extension into the 5' nontranslated regulatory region.

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The nucleic acid sequences and oligonucleotides of the invention can also be prepared by solid-phase methods, according to known synthetic methods. Typically, fragments of up to about 100 bases are individually synthesized, then joined to form continuous sequences up to several hundred bases.

5

B. Use of variant nucleic acid sequence for the production of variant products

In accordance with the present invention, nucleic acid sequences specified
10 above may be used as recombinant DNA molecules that direct the expression of variant products.

As will be understood by those of skill in the art, it may be advantageous to produce variant product-encoding nucleotide sequences possessing codons other than those which appear in any one of SEQ ID NO: 1 to SEQ ID NO: 87
15 which are those which naturally occur in the human genome. Codons preferred by a particular prokaryotic or eukaryotic host (Murray, E. *et al. Nuc Acids Res.*, 17:477-508, (1989)) can be selected, for example, to increase the rate of variant product expression or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, than transcripts produced from naturally
20 occurring sequence.

The nucleic acid sequences of the present invention can be engineered in order to alter a variant product coding sequence for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression of the product. For example, alterations may be introduced
25 using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, etc.

The present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs
30 comprise a vector, such as a plasmid or viral vector, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation.

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In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. Appropriate cloning and
5 expression vectors for use with prokaryotic and eukaryotic hosts are also described in Sambrook, *et al.*, (*supra*).

The present invention also relates to host cells which are genetically engineered with vectors of the invention, and the production of the product of the invention by recombinant techniques. Host cells are genetically engineered (i.e.,
10 transduced, transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the
15 expression of the variant nucleic acid sequence. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art.

The nucleic acid sequences of the present invention may be included in any one of a variety of expression vectors for expressing a product. Such vectors
20 include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and viable in the host.
25 The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and related sub-cloning procedures are deemed to be within the scope of those skilled in the art.

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The DNA sequence in the expression vector is operatively linked to an appropriate transcription control sequence (promoter) to direct mRNA synthesis. Examples of such promoters include: LTR or SV40 promoter, the *E.coli lac* or *trp* promoter, the phage lambda *PL* promoter, and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation, and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E.coli*.

The vector containing the appropriate DNA sequence as described above, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein. Examples of appropriate expression hosts include: bacterial cells, such as *E.coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila* and *Spodoptera Sf9*; animal cells such as CHO, COS, HEK 293 or Bowes melanoma; adenoviruses; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein. The invention is not limited by the host cells employed.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the variant product. For example, when large quantities of variant product are needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be desirable. Such vectors include, but are not limited to, multifunctional *E.coli* cloning and expression vectors such as *Bluescript(R)* (Stratagene), in which the variant polypeptide coding sequence may be ligated into the vector in-frame with sequences for the amino-terminal Met and the subsequent 7 residues of beta-galactosidase so that a hybrid protein is produced;

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pIN vectors (Van Heeke & Schuster *J. Biol. Chem.* **264**:5503-5509, (1989)); *pET* vectors (Novagen, Madison WI); and the like.

In the yeast *Saccharomyces cerevisiae* a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase and
5 PGH may be used. For reviews, see Ausubel *et al.* (*supra*) and Grant *et al.*, (*Methods in Enzymology* **153**:516-544, (1987)).

In cases where plant expression vectors are used, the expression of a sequence encoding variant product may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of
10 *CaMV* (Brisson *et al.*, *Nature* **310**:511-514, (1984)) may be used alone or in combination with the omega leader sequence from TMV (Takamatsu *et al.*, *EMBO J.*, **6**:307-311, (1987)). Alternatively, plant promoters such as the small subunit of RUBISCO (Coruzzi *et al.*, *EMBO J.* **3**:1671-1680, (1984); Broglie *et al.*, *Science* **224**:838-843, (1984)); or heat shock promoters (Winter J and
15 Sinibaldi R.M., *Results Probl. Cell Differ.*, **17**:85-105, (1991)) may be used. These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. For reviews of such techniques, see Hobbs S. or Murry L.E. (1992) in McGraw Hill Yearbook of Science and Technology, McGraw Hill, New York, N.Y., pp 191-196; or Weissbach and Weissbach (1988)
20 *Methods for Plant Molecular Biology*, Academic Press, New York, N.Y., pp 421-463.

Variant product may also be expressed in an insect system. In one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia*
25 larvae. The variant product coding sequence may be cloned into a nonessential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of variant coding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein coat. The recombinant viruses are then used to infect *S. frugiperda* cells or

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Trichoplusia larvae in which variant protein is expressed (Smith *et al.*, *J. Virol.* 46:584, (1983); Engelhard, E.K. *et al.*, *Proc. Nat. Acad. Sci.* 91:3224-7, (1994)).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, a
5 variant product coding sequence may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a nonessential E1 or E3 region of the viral genome will result in a viable virus capable of expressing variant protein in infected host cells (Logan and Shenk, *Proc. Natl. Acad. Sci.* 81:3655-59, (1984). In addition,
10 transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be required for efficient translation of a variant product coding sequence. These signals include the ATG initiation codon and adjacent sequences. In cases where variant product coding sequence,
15 its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon must be provided. Furthermore, the initiation codon must be in the correct
20 reading frame to ensure transcription of the entire insert. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate to the cell system in use (Scharf, D. *et al.*, (1994) *Results Probl. Cell Differ.*, 20:125-62, (1994); Bittner *et al.*, *Methods in*
25 *Enzymol* 153:516-544, (1987)).

In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell.
30 Introduction of the construct into the host cell can be effected by calcium

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phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis, L., Dibner, M., and Battey, I. (1986) Basic Methods in Molecular Biology). Cell-free translation systems can also be employed to produce polypeptides using RNAs derived from the DNA constructs of the present invention.

A host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the protein include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation. Post-translational processing which cleaves a "*pre-pro*" form of the protein may also be important for correct insertion, folding and/or function. Different host cells such as CHO, HeLa, MDCK, 293, WI38, etc. have specific cellular machinery and characteristic mechanisms for such post-translational activities and may be chosen to ensure the correct modification and processing of the introduced, foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express variant product may be transformed using expression vectors which contain viral origins of replication or endogenous expression elements and a selectable marker gene. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clumps of stably transformed cells can be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler M., *et al.*, *Cell* 11:223-32, (1977)) and adenine phosphoribosyltransferase (Lowy I., *et al.*, *Cell* 22:817-23, (1980)) genes which can be employed in *tk*- or *aprt*- cells, respectively. Also, antimetabolite,

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antibiotic or herbicide resistance can be used as the basis for selection; for example, *dhfr* which confers resistance to methotrexate (Wigler M., *et al.*, *Proc. Natl. Acad. Sci.* 77:3567-70, (1980)); *npt*, which confers resistance to the aminoglycosides neomycin and G-418 (Colbere-Garapin, F. *et al.*, *J. Mol. Biol.*, 5 150:1-14, (1981)) and *als* or *pat*, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, *trpB*, which allows cells to utilize indole in place of tryptophan, or *hisD*, which allows cells to utilize histinol in place of histidine (Hartman S.C. and R.C. Mulligan, *Proc. Natl. Acad. Sci.* 10 85:8047-51, (1988)). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate, GUS, and luciferase and its substrates, luciferin and ATP, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C.A. *et al.*, 15 *Methods Mol. Biol.*, 55:121-131, (1995)).

Host cells transformed with a nucleotide sequence encoding variant product may be cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The product produced by a recombinant cell may be secreted or contained intracellularly depending on the 20 sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing nucleic acid sequences encoding variant product can be designed with signal sequences which direct secretion of variant product through a prokaryotic or eukaryotic cell membrane.

The variant product may also be expressed as a recombinant protein with 25 one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS 30 extension/affinity purification system (Immunex Corp, Seattle, Wash.). The

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inclusion of a protease-cleavable polypeptide linker sequence between the purification domain and variant product is useful to facilitate purification. One such expression vector provides for expression of a fusion protein comprising a variant polypeptide fused to a polyhistidine region separated by an enterokinase
5 cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography, as described in Porath, *et al.*, *Protein Expression and Purification*, 3:263-281, (1992)) while the enterokinase cleavage site provides a means for isolating variant polypeptide from the fusion protein. *pGEX* vectors (Promega, Madison, Wis.) may also be used to express
10 foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to ligand-agarose beads (e.g., glutathione-agarose in the case of GST-fusions) followed by elution in the presence of free ligand.

Following transformation of a suitable host strain and growth of the host
15 strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification. Microbial cells employed in expression of proteins can
20 be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, or other methods, which are well known to those skilled in the art.

The variant products can be recovered and purified from recombinant cell cultures by any of a number of methods well known in the art, including
25 ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high

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performance liquid chromatography (HPLC) can be employed for final purification steps.

C. Diagnostic applications utilizing nucleic acid sequences

5 The nucleic acid sequences of the present invention may be used for a variety of diagnostic purposes. The nucleic acid sequences may be used to detect and quantitate expression of the variant in patient's cells, e.g. biopsied tissues, by detecting the presence of mRNA coding for variant product. Alternatively, the assay may be used to detect soluble variant in the serum or blood. This assay
10 typically involves obtaining total mRNA from the tissue or serum and contacting the mRNA with a nucleic acid probe. The probe is a nucleic acid molecule of at least 20 nucleotides, preferably 20-30 nucleotides, capable of specifically hybridizing with a sequence included within the sequence of a nucleic acid molecule encoding variant product under hybridizing conditions, detecting the
15 presence of mRNA hybridized to the probe, and thereby detecting the expression of variant. This assay can be used to distinguish between absence, presence, and excess expression of variant product and to monitor levels of variant expression during therapeutic intervention. In addition, the assay may be used to compare the levels of the variant of the invention to the levels of the original sequence from
20 which it has been varied or to levels of other variants, which comparison may have some physiological meaning.

The invention also contemplates the use of the nucleic acid sequences as a diagnostic for diseases resulting from inherited defective variant sequences, or diseases in which the ratio of the amount of the original sequence from which the
25 variant was varied to the novel variants of the invention is altered. These sequences can be detected by comparing the sequences of the defective (i.e., mutant) variant coding region with that of a normal coding region. Association of the sequence coding for mutant variant product with abnormal variant product activity may be verified. In addition, sequences encoding mutant variant products
30 can be inserted into a suitable vector for expression in a functional assay system

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(e.g., colorimetric assay, complementation experiments in a variant protein deficient strain of HEK293 cells) as yet another means to verify or identify mutations. Once mutant genes have been identified, one can then screen populations of interest for carriers of the mutant gene.

5 Individuals carrying mutations in the nucleic acid sequence of the present invention may be detected at the DNA level by a variety of techniques. Nucleic acids used for diagnosis may be obtained from a patient's cells, including but not limited to such as from blood, urine, saliva, placenta, tissue biopsy and autopsy material. Genomic DNA may be used directly for detection or may be amplified
10 enzymatically by using PCR (Saiki, *et al.*, *Nature* 324:163-166, (1986)) prior to analysis. RNA or cDNA may also be used for the same purpose. As an example, PCR primers complementary to the nucleic acid of the present invention can be used to identify and analyze mutations in the gene of the present invention. Deletions and insertions can be detected by a change in size of the amplified
15 product in comparison to the normal genotype.

Point mutations can be identified by hybridizing amplified DNA to radiolabeled RNA of the invention or alternatively, radiolabeled antisense DNA sequences of the invention. Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the
20 chemical cleavage method (e.g. Cotton, *et al.* *Proc. Natl. Acad. Sci. USA*, 85:4397-4401, (1988)), or by differences in melting temperatures. "Molecular beacons" (Kostrikis L.G. *et al.*, *Science* 279:1228-1229, (1998)), hairpin-shaped, single-stranded synthetic oligo- nucleotides containing probe sequences which are complementary to the nucleic acid of the present invention, may also be used
25 to detect point mutations or other sequence changes as well as monitor expression levels of variant product. Such diagnostics would be particularly useful for prenatal testing.

Another method for detecting mutations uses two DNA probes which are designed to hybridize to adjacent regions of a target, with abutting bases, where
30 the region of known or suspected mutation(s) is at or near the abutting bases.

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The two probes may be joined at the abutting bases, e.g., in the presence of a ligase enzyme, but only if both probes are correctly base paired in the region of probe junction. The presence or absence of mutations is then detectable by the presence or absence of ligated probe.

5 Also suitable for detecting mutations in the variant product coding sequence are oligonucleotide array methods based on sequencing by hybridization (SBH), as described, for example, in U.S. Patent No. 5,547,839. In a typical method, the DNA target analyte is hybridized with an array of oligonucleotides formed on a microchip. The sequence of the target can then be
10 "read" from the pattern of target binding to the array.

D. Gene mapping utilizing nucleic acid sequences

The nucleic acid sequences of the present invention are also valuable for chromosome identification. The sequence is specifically targeted to and can
15 hybridize with a particular location on an individual human chromosome. Moreover, there is a current need for identifying particular sites on the chromosome. Few chromosome marking reagents based on actual sequence data (repeat polymorphisms) are presently available for marking chromosomal location. The mapping of DNAs to chromosomes according to the present
20 invention is an important first step in correlating those sequences with genes associated with disease.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 20-30 bp) from the variant cDNA. Computer analysis of the 3' untranslated region is used to rapidly select primers that do not span more than
25 one exon in the genomic DNA, which would complicate the amplification process. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the primer will yield an amplified fragment.

PCR mapping of somatic cell hybrids or using instead radiation hybrids
30 are rapid procedures for assigning a particular DNA to a particular chromosome.

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Using the present invention with the same oligonucleotide primers, sublocalization can be achieved with panels of fragments from specific chromosomes or pools of large genomic clones in an analogous manner. Other mapping strategies that can similarly be used to map to its chromosome include *in situ* hybridization, prescreening with labeled flow-sorted chromosomes and preselection by hybridization to construct chromosome specific-cDNA libraries.

Fluorescence *in situ* hybridization (FISH) of a cDNA clone to a metaphase chromosomal spread can be used to provide a precise chromosomal location in one step. This technique can be used with cDNA as short as 50 or 60 bases. For a review of this technique, see Verma *et al.*, *Human Chromosomes: a Manual of Basic Techniques*, (1988) Pergamon Press, New York.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, for example, in the OMIM database (Center for Medical Genetics, Johns Hopkins University, Baltimore, MD and National Center for Biotechnology Information, National Library of Medicine, Bethesda, MD). The OMIM gene map presents the cytogenetic map location of disease genes and other expressed genes. The OMIM database provides information on diseases associated with the chromosomal location. Such associations include the results of linkage analysis mapped to this interval, and the correlation of translocations and other chromosomal aberrations in this area with the advent of polygenic diseases, such as cancer, in general and prostate cancer in particular.

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E. Therapeutic applications of nucleic acid sequences

Nucleic acid sequences of the invention may also be used for therapeutic purposes. Turning first to the second aspect of the invention (i.e. inhibition of expression of variant), expression of variant product may be modulated through antisense technology, which controls gene expression through hybridization of complementary nucleic acid sequences, i.e. antisense DNA or RNA, to the control, 5' or regulatory regions of the gene encoding variant product. For example, the 5' coding portion of the nucleic acid sequence sequence which codes for the product of the present invention is used to design an antisense oligonucleotide of from about 10 to 40 base pairs in length. Oligonucleotides derived from the transcription start site, e.g. between positions -10 and +10 from the start site, are preferred. An antisense DNA oligonucleotide is designed to be complementary to a region of the nucleic acid sequence involved in transcription (Lee *et al.*, *Nucl. Acids, Res.*, 6:3073, (1979); Cooney *et al.*, *Science* 241:456, (1988); and Dervan *et al.*, *Science* 251:1360, (1991)), thereby preventing transcription and the production of the variant products. An antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the variant products (Okano *J. Neurochem.* 56:560, (1991)). The antisense constructs can be delivered to cells by procedures known in the art such that the antisense RNA or DNA may be expressed *in vivo*. The antisense may be antisense mRNA or DNA sequence capable of coding such antisense mRNA. The antisense mRNA or the DNA coding thereof can be complementary to the full sequence of nucleic acid sequences coding for the variant protein or to a fragment of such a sequence which is sufficient to inhibit production of a protein product.

Turning now to the first aspect of the invention, i.e. expression of variant, expression of variant product may be increased by providing coding sequences for coding for said product under the control of suitable control elements ending its expression in the desired host.

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The nucleic acid sequences of the invention may be employed in combination with a suitable pharmaceutical carrier. Such compositions comprise a therapeutically effective amount of the compound, and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The formulation should suit the mode of administration.

The products of the invention as well as any activators and deactivators compounds (see below) which are polypeptides, may also be employed in accordance with the present invention by expression of such polypeptides *in vivo*, which is often referred to as "*gene therapy*." Cells from a patient may be engineered with a nucleic acid sequence (DNA or RNA) encoding a polypeptide *ex vivo*, with the engineered cells then being provided to a patient to be treated with the polypeptide. Such methods are well-known in the art. For example, cells may be engineered by procedures known in the art by use of a retroviral particle containing RNA encoding a polypeptide of the present invention.

Similarly, cells may be engineered *in vivo* for expression of a polypeptide *in vivo* by procedures known in the art. As known in the art, a producer cell for producing a retroviral particle containing RNA encoding the polypeptide of the present invention may be administered to a patient for engineering cells *in vivo* and expression of the polypeptide *in vivo*. These and other methods for administering a product of the present invention by such method should be apparent to those skilled in the art from the teachings of the present invention. For example, the expression vehicle for engineering cells may be other than a retrovirus, for example, an adenovirus which may be used to engineer cells *in vivo* after combination with a suitable delivery vehicle.

Retroviruses from which the retroviral plasmid vectors mentioned above may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, adenovirus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

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The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the *PE501*, *PA317*, *psi-2*, *psi-AM*, *PA12*, *T19-14X*, *VT-19-17-H2*, *psi-CRE*, *psi-CRIP*, *GP+E-86*, *GP+envAm12*,
5 and *DAN* cell lines as described in Miller (*Human Gene Therapy*, Vol. 1, pg. 5-14, (1990)). The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO_4 precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a
10 lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include the nucleic acid sequence(s) encoding the polypeptides. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either *in vitro* or *in vivo*. The transduced eukaryotic cells will express the nucleic
15 acid sequence(s) encoding the polypeptide. Eukaryotic cells which may be transduced include, but are not limited to, embryonic stem cells, embryonic carcinoma cells, as well as hematopoietic stem cells, hepatocytes, fibroblasts, myoblasts, keratinocytes, endothelial cells, and bronchial epithelial cells.

The genes introduced into cells may be placed under the control of
20 inducible promoters, such as the radiation-inducible *Egr-1* promoter, (Maceri, H.J., *et al.*, *Cancer Res.*, 56(19):4311 (1996)), to stimulate variant production or antisense inhibition in response to radiation, eg., radiation therapy for treating tumors.

25 **Example III. Variant product**

The substantially purified variant product of the invention has been defined above as the product coded from the nucleic acid sequence of the invention. Preferably the amino acid sequence is an amino acid sequence having at least 90% identity to any one of the sequences identified as SEQ ID NO: 88 to
30 SEQ ID NO: 174 provided that the amino acid sequence is not identical to that of

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the original sequence from which it has been varied. The protein or polypeptide may be in mature and/or modified form, also as defined above. Also contemplated are protein fragments having at least 10 contiguous amino acid residues, preferably at least 10-20 residues, derived from the variant product, as well as homologues as explained above.

The sequence variations are preferably those that are considered conserved substitutions, as defined above. Thus, for example, a protein with a sequence having at least 90% sequence identity with any of the products identified as SEQ ID NO: 88 to SEQ ID NO: 174, preferably by utilizing conserved substitutions as defined above is also part of the invention, and provided that it is not identical to the original peptide from which it has been varied. In a more specific embodiment, the protein has or contains any one of the sequence identified as SEQ ID NO: 88 to SEQ ID NO: 174. The variant product may be (i) one in which one or more of the amino acid residues in a sequence listed above are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue), or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the variant product is fused with another compound, such as a compound to increase the half-life of the protein (for example, polyethylene glycol (PEG)), or a moiety which serves as targeting means to direct the protein to its target tissue or target cell population (such as an antibody), or (iv) one in which additional amino acids are fused to the variant product. Such fragments, variants and derivatives are deemed to be within the scope of those skilled in the art from the teachings herein.

25 A. Preparation of variant product

Recombinant methods for producing and isolating the variant product, and fragments of the protein are described above.

In addition to recombinant production, fragments and portions of variant product may be produced by direct peptide synthesis using solid-phase techniques (cf. Stewart *et al.*, (1969) Solid-Phase Peptide Synthesis, WH Freeman Co, San

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Francisco; Merrifield J., *J. Am. Chem. Soc.*, 85:2149-2154, (1963)). In vitro peptide synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer, Foster City, Calif.) in accordance with
5 the instructions provided by the manufacturer. Fragments of variant product may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

B. Therapeutic uses and compositions utilizing the variant product

10

The variant product of the invention is generally useful in treating diseases and disorders which are characterized by a lower than normal level of variant expression, and or diseases which can be cured or ameliorated by raising the level of the variant product, even if the level is normal.

15

Variant products or fragments may be administered by any of a number of routes and methods designed to provide a consistent and predictable concentration of compound at the target organ or tissue. The product-containing compositions may be administered alone or in combination with other agents, such as stabilizing compounds, and/or in combination with other pharmaceutical
20 agents such as drugs or hormones.

Variant product-containing compositions may be administered by a number of routes including, but not limited to oral, intravenous, intramuscular, transdermal, subcutaneous, topical, sublingual, or rectal means as well as by nasal application. Variant product-containing compositions may also be administered
25 via liposomes. Such administration routes and appropriate formulations are generally known to those of skill in the art.

The product can be given via intravenous or intraperitoneal injection. Similarly, the product may be injected to other localized regions of the body. The product may also be administered via nasal insufflation. Enteral administration is
30 also possible. For such administration, the product should be formulated into an

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appropriate capsule or elixir for oral administration, or into a suppository for rectal administration.

The foregoing exemplary administration modes will likely require that the product be formulated into an appropriate carrier, including ointments, gels, 5 suppositories. Appropriate formulations are well known to persons skilled in the art.

Dosage of the product will vary, depending upon the potency and therapeutic index of the particular polypeptide selected.

A therapeutic composition for use in the treatment method can include the 10 product in a sterile injectable solution, the polypeptide in an oral delivery vehicle, the product in an aerosol suitable for nasal administration, or the product in a nebulized form, all prepared according to well known methods. Such compositions comprise a therapeutically effective amount of the compound, and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not 15 limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The product of the invention may also be used to modulate endothelial differentiation and proliferation as well as to modulate apoptosis either *ex vivo* or *in vitro*, for example, in cell cultures.

20 **Example IV. Screening methods for activators and deactivators (inhibitors)**

The present invention also includes an assay for identifying molecules, such as synthetic drugs, antibodies, peptides, or other molecules, which have a modulating effect on the activity of the variant product, e.g. activators or 25 deactivators of the variant product of the present invention. Such an assay comprises the steps of providing an variant product encoded by the nucleic acid sequences of the present invention, contacting the variant protein with one or more candidate molecules to determine the candidate molecules modulating effect on the activity of the variant product, and selecting from the molecules a 30 candidate's molecule capable of modulating variant product physiological activity.

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The variant product, its catalytic or immunogenic fragments or oligopeptides thereof, can be used for screening therapeutic compounds in any of a variety of drug screening techniques. The fragment employed in such a test may be free in solution, affixed to a solid support, borne on a cell membrane or
5 located intracellularly. The formation of binding complexes, between variant product and the agent being tested, may be measured. Alternatively, the activator or deactivator may work by serving as agonist or antagonist, respectively, of the variant receptor, binding entity or target site, and their effect may be determined in connection with any of the above.

10 Another technique for drug screening which may be used provides for high throughput screening of compounds having suitable binding affinity to the variant product is described in detail by Geysen in PCT Application WO 84/03564, published on Sep. 13, 1984. In summary, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic
15 pins or some other surface. The peptide test compounds are reacted with the full variant product or with fragments of variant product and washed. Bound variant product is then detected by methods well known in the art. Substantially purified variant product can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing
20 antibodies can be used to capture the peptide and immobilize it on a solid support.

Antibodies to the variant product, as described in Example VI below, may also be used in screening assays according to methods well known in the art. For example, a "sandwich" assay may be performed, in which an anti-variant
25 antibody is affixed to a solid surface such as a microtiter plate and variant product is added. Such an assay can be used to capture compounds which bind to the variant product. Alternatively, such an assay may be used to measure the ability of compounds to influence with the binding of variant product to the variant receptor, and then select those compounds which effect the binding.

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Example V. Anti-variant antibodies**A. Synthesis**

In still another aspect of the invention, the purified variant product is used to produce anti-variant antibodies which have diagnostic and therapeutic uses
5 related to the activity, distribution, and expression of the variant product.

Antibodies to the variant product may be generated by methods well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, humanized, single chain, Fab fragments and fragments produced by an Fab expression library. Antibodies, i.e., those which inhibit
10 dimer formation, are especially preferred for therapeutic use.

A fragment of the variant product for antibody induction does not require biological activity but have to feature immunological activity; however, the protein fragment or oligopeptide must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five
15 amino acids, preferably at least 10 amino acids of the sequences specified in any one of SEQ ID NO: 88 to SEQ ID NO: 174. Preferably they should mimic a portion of the amino acid sequence of the natural protein and may contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of variant protein amino acids may be fused with those of another
20 protein such as keyhole limpet hemocyanin and antibody produced against the chimeric molecule. Procedures well known in the art can be used for the production of antibodies to variant product.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, etc may be immunized by injection with variant product or any
25 portion, fragment or oligopeptide which retains immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include but are not limited to Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet

hemocyanin, and dinitrophenol. BCG (bacilli Calmette-Guerin) and *Corynebacterium parvum* are potentially useful human adjuvants.

Monoclonal antibodies to variant protein may be prepared using any technique which provides for the production of antibody molecules by continuous
5 cell lines in culture. These include but are not limited to the hybridoma technique originally described by Koehler and Milstein (*Nature* 256:495-497, (1975)), the human B-cell hybridoma technique (Kosbor *et al.*, *Immunol. Today* 4:72, (1983); Cote *et al.*, *Proc. Natl. Acad. Sci.* 80:2026-2030, (1983)) and the EBV-hybridoma technique (Cole, *et al.*, *Mol. Cell Biol.* 62:109-120, (1984)).

10 Techniques developed for the production of "chimeric antibodies", the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity can also be used (Morrison *et al.*, *Proc. Natl. Acad. Sci.* 81:6851-6855, (1984); Neuberger *et al.*, *Nature* 312:604-608, (1984); Takeda *et al.*, *Nature* 314:452-454, (1985)).
15 Alternatively, techniques described for the production of single chain antibodies (U.S. Pat. No. 4,946,778) can be adapted to produce single-chain antibodies specific for the variant protein.

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening recombinant immunoglobulin libraries or
20 panels of highly specific binding reagents as disclosed in Orlandi *et al.* (*Proc. Natl. Acad. Sci.* 86:3833-3837, 1989)), and Winter G and Milstein C., (*Nature* 349:293-299, (1991)).

Antibody fragments which contain specific binding sites for variant protein may also be generated. For example, such fragments include, but are not
25 limited to, the F(ab')₂ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse W.D. *et al.*, *Science*
30 256:1275-1281, (1989)).

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B. Diagnostic applications of antibodies

A variety of protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the formation of complexes between the variant product and its specific antibody and the measurement of complex formation. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two noninterfering epitopes on a specific variant product is preferred, but a competitive binding assay may also be employed. These assays are described in Maddox D.E., *et al.*, 10 (*J. Exp. Med.* **158**:1211, (1983)).

Antibodies which specifically bind variant product are useful for the diagnosis of conditions or diseases characterized by expression of the novel variant of the invention (where normally it is not expressed) by over or under expression of variant as well as for detection of diseases in which the proportion between the amount of the variants of the invention and the original sequence from which it varied is altered. Alternatively, such antibodies may be used in assays to monitor patients being treated with variant product, its activators, or its deactivators. Diagnostic assays for variant protein include methods utilizing the antibody and a label to detect variant product in human body fluids or extracts of 15 cells or tissues. The products and antibodies of the present invention may be used with or without modification. Frequently, the proteins and antibodies will be labeled by joining them, either covalently or noncovalently, with a reporter molecule. A wide variety of reporter molecules are known in the art.

A variety of protocols for measuring the variant product, using either 25 polyclonal or monoclonal antibodies specific for the respective protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescent activated cell sorting (FACS). As noted above, a two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on variant product is preferred, but a competitive binding assay may be employed. These assays are 30

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described, among other places, in Maddox, *et al.* (*supra*). Such protocols provide a basis for diagnosing altered or abnormal levels of variant product expression. Normal or standard values for variant product expression are established by combining body fluids or cell extracts taken from normal subjects, preferably
5 human, with antibody to variant product under conditions suitable for complex formation which are well known in the art. The amount of standard complex formation may be quantified by various methods, preferably by photometric methods. Then, standard values obtained from normal samples may be compared with values obtained from samples from subjects potentially affected by disease.
10 Deviation between standard and subject values establishes the presence of disease state.

The antibody assays are useful to determine the level of variant product present in a body fluid sample, in order to determine whether it is being expressed at all, whether it is being overexpressed or underexpressed in the
15 tissue, or as an indication of how variant levels of variable products are responding to drug treatment.

By another aspect the invention concerns methods for determining the presence or level of various anti-variant antibodies in a biological sample obtained from patients, such as blood or serum sample using as an antigen the
20 variant product. Determination of said antibodies may be indicative to a plurality of pathological conditions or diseases.

C. Therapeutic uses of antibodies

In addition to their diagnostic use the antibodies may have a therapeutical
25 utility in blocking or decreasing the activity of the variant product in pathological conditions where beneficial effect can be achieved by such a decrease.

The antibody employed is preferably a humanized monoclonal antibody, or a human Mab produced by known globulin-gene library methods. The antibody is administered typically as a sterile solution by IV injection, although
30 other parenteral routes may be suitable. Typically, the antibody is administered

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in an amount between about 1-15 mg/kg body weight of the subject. Treatment is continued, e.g., with dosing every 1-7 days, until a therapeutic improvement is seen.

Although the invention has been described with reference to specific
5 methods and embodiments, it is appreciated that various modifications and changes may be made without departing from the invention.

Example VI. Expression of ACEV

(a) Immunohistochemical staining:

The immunohistochemical staining was performed using Histostain plus Kit
10 (Zymed Laboratories Inc.). Mouse salivary gland micron sections were prepared using a R. Gung microtome and fixed on superfrost plus slides with 2% Tespa. Deparaffinization was performed in xylene for 10 min. Dehydration was performed three times in absolute ethanol and once 95% ethanol. The slides were washed in DDW and then incubated with 3% H₂O for 5 min. Subsequently, the slide were washed in
15 DDW and twice in 0.05M TrisHCl pH 7.6 (Optimax wash Buffer, BioGenex). The rest of the procedure was performed following the manufacturer's instructions. The results are shown in Figs. 88 and 89.

The immunohistochemical staining was performed on mouse salivary gland
20 micron sections. The immunohistochemistry was done using specific polyclonal antibodies designed against the c-terminus of SEQ ID NO: 144 (12 amino-acids), which are unique to said ACEV product and lack in the original ACE protein (Fig 88-a,b,d magnification X 100; Fig 89-b magnification X 400) compared with the pre-immune rabbit's serum (Fig 88-c, Fig. 89-a).

25 ACE was found to express in ductal epifilus (Fig 88-a,b,d, Fig 89-b).

The same procedure was repeated for mouse lymph node sectors stained with pre-immune serum (Fig. 90a, 90c – magnifications X 100, X 200, respectively) and immune serum (Fig. 90b and 90c magnifications X 100, X 200 respectively).

The results show positive staining in salivary glands.

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(b) RT - PCR

RNA Purification and cDNA Synthesis Total RNA was extracted from different mouse tissues using Tri-Reagent System (Molecular Research Center, Inc., Cincinnati, OH). Synthesis of first-strand cDNA was carried out using Oligo(dT)15 (Promega, 5 Madison, WI), Superscript II (Gibco/BRL, Gaithersburg, MD), Rnasin (Promega, Madison, WI) and dNTP's (Gibco/BRL, Gaithersburg, MD). + with Superscript II, - without Superscript II.

Polymerase Chain Reaction (PCR): PCR was performed using Expand Long Template PCR system (Roche). As a template cDNA from different tissues was used. 10 The PCR reaction on PTC-225 (MJ Research, Inc.). PCR products were analyzed on an automated DNA sequencer ABI Prizem 310 Genetic Analyzer (Perkin Elmer).

The results are shown in Fig. 91. As can be seen the ACEV of the invention was expressed in skin, lung, heart, thymus, spleen, bone marrow and brain tissue

CLAIMS:

1. An isolated nucleic acid sequence, of an alternative splicing variant, selected from the group consisting of:
 - (i) the nucleic acid sequence depicted in any one of SEQ ID NO: 1 to
5 SEQ ID NO: 87;
 - (ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and
 - 10 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.
2. An isolated nucleic acid sequence complementary to the nucleic acid
15 sequence of Claim 1.
3. An amino acid sequence selected from the group consisting of:
 - (i) an amino acid sequence coded by the isolated nucleic acid sequence of alternative splice variants of Claim 1;
 - (ii) homologues of the amino acid sequences of (i) in which one or more
20 amino acids has been added, deleted, replaced or chemically modified in the region or adjacent to the region where the amino acid sequences differs from the original amino acid sequence, coded by the original nucleic acid sequence from which the variant has been varied.
- 25 4. An amino acid sequence according to Claim 3, as depicted in any one of SEQ ID NO: 88 to SEQ ID NO: 174.
5. An isolated nucleic acid sequence coding for any one of the amino acid sequences of Claim 3 or 4.
6. A purified antibody which binds specifically to any of the amino acid
30 sequence of Claim 3 or 4.

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7. An expression vector comprising any one of the nucleic acid sequences of Claim 1 or 5 and control elements for the expression of the nucleic acid sequence in a suitable host.
8. An expression vector comprising any one of the nucleic acid sequences of Claim 2, and control elements for the expression of the nucleic acid sequences in a suitable host.
9. A host cell transfected by the expression vector of Claim 7 or 8.
10. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:
 - (i) the expression vector of Claim 7; and
 - (ii) any one of the amino acid sequences of Claim 3 or 4.
11. A pharmaceutical composition according to Claim 10, for treatment of diseases which can be ameliorated or cured by raising the level of any one of the amino acid sequences depicted in SEQ ID NO: 88 to SEQ ID NO: 174.
12. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:
 - (i) any one of the nucleic acid sequences of Claim 2;
 - (ii) the expression vector of Claim 8; and
 - (iii) the purified antibody of Claim 6.
13. A pharmaceutical composition according to Claim 12, for treatment of diseases which can be ameliorated or cured by decreasing the level of any one of the amino acid sequences depicted in SEQ ID NO: 88 to SEQ ID NO: 174.
14. A method for detecting an variant nucleic acid sequence in a biological sample, comprising the steps of:
 - (a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 1 or 2; and
 - (b) detecting said hybridization complex;wherein the presence of said hybridization complex correlates with the presence of an variant nucleic acid sequence in the said biological sample.
15. A method for determining the level of variant nucleic acid sequences in a biological sample comprising the steps of:

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(a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 1 or 2; and

(b) determining the amount of hybridization complexes and normalizing said amount to provide the level of the variant nucleic acid sequences in the sample.

16. A method for determining the ratio between the level of variant of the nucleic acid sequence in a first biological sample and the level of the original sequence from which the variant has been varied by alternative splicing in a second biological sample comprising:

10 (a) determining the level of the variant nucleic acid sequence in the first biological sample according to the method of Claim 15;

(b) determining the level of the original sequence in the second biological sample; and

(c) comprising the levels obtained in (a) and (b) to give said ratio.

15 17. A method according to Claim 16, wherein said first and said second biological samples are the same sample.

18. A method according to any of Claims 14 to 17, wherein the nucleic acid material of said biological sample are mRNA transcripts.

19. A method according to Claim 18, where the nucleic acid sequence is present in a nucleic acid chip.

20. A method for identifying candidate compounds capable of binding to the variant product and modulating its activity the method comprising:

(i) providing any one of the amino acid sequences as defined in Claim 3 or 4;

25 (ii) contacting a candidate compound with said amino acid sequence;

(iii) determining the effect of said candidate compound on the biological activity of said protein or polypeptide and selecting those compounds which show a significant effect on said biological activity.

21. A method according to Claim 20, wherein the compound is an activator and the measured effect is increase in the biological activity.

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22. A method according to Claim 20, wherein the compound is an deactivator and the effect is decrease in the biological activity.
23. An activator of any one of the amino acid sequences of Claim 3 or 4.
24. An deactivator of any one of the amino acid sequences of Claims 3 or 4.
- 5 25. A method for detecting any one of the amino acid sequences of Claim 3 or 4 in a biological sample, comprising the steps of:
- (a) contacting with said biological sample the antibody of Claim 8, thereby forming an antibody-antigen complex; and
 - (b) detecting said antibody-antigen complex
- 10 wherein the presence of said antibody-antigen complex correlates with the presence of the desired amino acid in said biological sample.
26. A method for detecting the level of the amino acid sequence of any one of Claim 3 or 4 in a biological sample, comprising the steps of:
- (a) contacting with said biological sample the antibody of Claim 8,
- 15 thereby forming an antibody-antigen complex; and
- (b) detecting the amount of said antibody-antigen complex and normalizing said amount to provide the level of said amino acid sequence in the sample.
27. A method for determining the ratio between the level of any one of the
- 20 amino acid sequences of Claims 3 or 4 present in a first biological sample and the level of the original amino acid sequences from which they were varied by alternative splicing, present in a second biological sample, the method comprising:
- (a) determining the level of the amino acid sequences of Claims 3 or 4 into a first sample by the method of Claim 26;
- 25 (b) determining the level of the original amino acid sequence in the second sample; and
- (c) comparing the level obtained in (a) and (b) to give said ratio.
28. A method according to Claim 27, wherein said first and said second biological samples are the same sample.
- 30 29. A method for detecting any one of the antibodies of Claim 6 in a biological sample comprising the steps of:

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(a) contacting said biological sample with any one of the amino acid sequences of Claim 3 or 4 thereby forming an antibody-antigen complex; and

(b) detecting said antibody-antigen complex

wherein the presence of said antibody-antigen complex correlates with the presence of the antibody in said biological sample.

30. A method for detecting the level of any one of the antibodies of Claim 6 in a biological sample comprising the steps of:

(a) contacting said biological sample with any one of the amino acid sequences of Claim 3;

10 (b) detecting the amount of said antibody-antigen complex and normalizing said amount to provide the levels of said antibody in the sample.

31. An isolated nucleic acid sequence according to Claim 1 of an alternative splicing variant of an angiotensin converting enzyme (ACEV) selected from the group consisting of:

15 (i) the nucleic acid sequence depicted in SEQ ID NO: 57 or SEQ ID NO: 85;

(ii) nucleic acid sequences having at least 90% identity with the sequence of (i) with the proviso that each sequence is different than the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing; and

20 (iii) fragments of (i) or (ii) of at least 20 b.p., provided that said fragment contains a sequence which is not present, as a continuous stretch of nucleotides, in the original nucleic acid sequence from which the sequences of (i) have been varied by alternative splicing.

25 32. An isolated nucleic acid sequence complementary to the nucleic acid sequence of Claim 31.

33. An amino acid sequence selected from the group consisting of:

(i) an amino acid sequence coded by the isolated nucleic acid sequence of alternative splice variants of Claim 31;

30 (ii) homologues of the amino acid sequences of (i) in which one or more amino acids has been added, deleted, replaced or chemically modified in the region

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or adjacent to the region where the amino acid sequences differs from the original amino acid sequence, coded by the original nucleic acid sequence from which the variant has been varied.

34. An amino acid sequence according to Claim 33, as depicted in SEQ ID NO:
5 144 or SEQ ID NO: 172.

35. An isolated nucleic acid sequence coding for any one of the amino acid sequences of Claim 33 or 34.

36. A purified antibody which binds specifically to any of the amino acid sequence of Claim 33 or 34.

10 37. An expression vector comprising any one of the nucleic acid sequences of Claim 31 or 35 and control elements for the expression of the nucleic acid sequence in a suitable host.

38. An expression vector comprising any one of the nucleic acid sequences of Claim 32, and control elements for the expression of the nucleic acid sequences in a
15 suitable host.

39. A host cell transfected by the expression vector of Claim 37 or 38.

40. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and as an active ingredient an agent selected from the group consisting of:

- (i) the expression vector of Claim 37; and
- 20 (ii) any one of the amino acid sequences of Claim 33 or 34.

41. A pharmaceutical composition according to Claim 40, for treatment of diseases which can be ameliorated or cured by raising the level of any one of the amino acid sequences depicted in SEQ ID NO: 144 or SEQ ID NO: 172.

42. A pharmaceutical composition comprising a pharmaceutically acceptable
25 carrier and as an active ingredient an agent selected from the group consisting of:

- (i) any one of the nucleic acid sequences of Claim 32;
- (ii) the expression vector of Claim 38; and
- (iii) the purified antibody of Claim 36.

43. A pharmaceutical composition according to Claim 42, for treatment of
30 diseases which can be ameliorated or cured by decreasing the level of the amino acid sequences depicted in SEQ ID NO: 144 or SEQ ID NO: 172.

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44. A pharmaceutical composition according to Claim 40 or 42 for the treatment of a disease selected from: cardiovascular disorders, congestive heart failure, hypertension, renal hypertension, diabetes, multiple sclerosis, sarcoidosis, nonsarcoidotic pulmonary granulomatous diseases, vascular pathologies involving
5 an endothelial abnormality and cancer.

45. A method for detecting an variant nucleic acid sequence in a biological sample, comprising the steps of:

(a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 31 or 32; and

10 (b) detecting said hybridization complex;

wherein the presence of said hybridization complex correlates with the presence of an variant nucleic acid sequence in the said biological sample.

46. A method for determining the level of variant nucleic acid sequences in a biological sample comprising the steps of:

15 (a) hybridizing to nucleic acid material of said biological sample any one of the nucleic acid sequences of Claim 31 or 32; and

(b) determining the amount of hybridization complexes and normalizing said amount to provide the level of the variant nucleic acid sequences in the sample.

20 47. A method for determining the ratio between the level of variant of the nucleic acid sequence in a first biological sample and the level of the original sequence from which the variant has been varied by alternative splicing in a second biological sample comprising:

(a) determining the level of the variant nucleic acid sequence in the first
25 biological sample according to the method of Claim 46;

(b) determining the level of the original sequence in the second biological sample; and

(c) comprising the levels obtained in (a) and (b) to give said ratio.

48. A method according to Claim 47, wherein said first and said second
30 biological samples are the same sample.

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49. A method according to any of Claims 45 to 48, wherein the nucleic acid material of said biological sample are mRNA transcripts.
50. A method according to Claim 49, where the nucleic acid sequence is present in a nucleic acid chip.
- 5 51. A method for identifying candidate compounds capable of binding to the variant product and modulating its activity the method comprising:
- (i) providing any one of the amino acid sequences as defined in Claim 33 or 34;
 - (ii) contacting a candidate compound with said amino acid sequence;
 - 10 (iii) determining the effect of said candidate compound on the biological activity of said protein or polypeptide and selecting those compounds which show a significant effect on said biological activity.
52. A method according to Claim 51, wherein the compound is an activator and the measured effect is increase in the biological activity.
- 15 53. A method according to Claim 51, wherein the compound is an deactivator and the effect is decrease in the biological activity.
54. An activator of any one of the amino acid sequences of Claim 33 or 34.
55. An deactivator of any one of the amino acid sequences of Claims 33 or 34.
56. A method for detecting any one of the amino acid sequences of Claim 33 or 20 34 in a biological sample, comprising the steps of:
- (a) contacting with said biological sample the antibody of Claim 38, thereby forming an antibody-antigen complex; and
 - (b) detecting said antibody-antigen complex
- wherein the presence of said antibody-antigen complex correlates with the 25 presence of the desired amino acid in said biological sample.
57. A method for detecting the level of the amino acid sequence of any one of Claim 33 or 34 in a biological sample, comprising the steps of:
- (a) contacting with said biological sample the antibody of Claim 38, thereby forming an antibody-antigen complex; and

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(b) detecting the amount of said antibody-antigen complex and normalizing said amount to provide the level of said amino acid sequence in the sample.

58. A method for determining the ratio between the level of any one of the amino acid sequences of Claims 33 or 34 present in a first biological sample and the level of the original amino acid sequences from which they were varied by alternative splicing, present in a second biological sample, the method comprising:

(a) determining the level of the amino acid sequences of Claims 33 or 34 into a first sample by the method of Claim 57;

10 (b) determining the level of the original amino acid sequence in the second sample; and

(c) comparing the level obtained in (a) and (b) to give said ratio.

59. A method according to Claim 58, wherein said first and said second biological samples are the same sample.

15 60. A method for detecting any one of the antibodies of Claim 36 in a biological sample comprising the steps of:

(a) contacting said biological sample with any one of the amino acid sequences of Claim 3 or 4 thereby forming an antibody-antigen complex; and

(b) detecting said antibody-antigen complex

20 wherein the presence of said antibody-antigen complex correlates with the presence of the antibody in said biological sample.

61. A method for detecting the level of any one of the antibodies of Claim 36 in a biological sample comprising the steps of:

(a) contacting said biological sample with any one of the amino acid sequences of Claim 33;

(b) detecting the amount of said antibody-antigen complex and normalizing said amount to provide the levels of said antibody in the sample.

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1 MPIMGSSVYITVELAIAVLAILGNVLVCWAVWLSNLTQNVNTNYFVVS LAA 50
|||||
1 MPIMGSSVYITVELAIAVLAILGNVLVCWAVWLSNLTQNVNTNYFVVS LAA 50

51 ADI AVGV LAI PF AIT ISTGFCAACHGCLFIACFVLVLTQSSIFSLLAIAI 100
|||||
51 ADI AVGV LAI PF AIT ISTGFCAACHGCLFIACFVLVLTQSSIFSLLAIAI 100

101 DRYIAIRIPLRYNGLVTGTRAKGIIAICWVLSFAIGLTPMLGWNNCGQPK 150
|||||
101 DRYIAIRIPLRYNGLVTGTRAKGIIAICWVLSFAIGLTPMLGWNNCGQPK 150

151 EGKNHSQCGEGQVACLFEDVVP MN YMFNF FACVLVPLLLMLGVYLRI 200
|||||
151 EGKNHSQCGEGQVACLFEDVVP MN YMFNF FACVLVPLLLMLGVYLRI 200

201 FLAARRQLKQMESQPLPGERARSTLQKEVHAAKSLA.....PLH 239
|||||
201 FLAARRQLKQMESQPLPGERARSTLQKEVHAAKSLAIVGLFALCWLPLH 250

FIG. 1

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1 MPRYGASLRQSCPRSGREQQDGTAGAPGLLWMGLVLALALALALALSDS 90
|||||
1 MPRYGASLRQSCPRSGREQQDGTAGAPGLLWMG..LALALALALALSDS 48
.
91 RVLWAPAEAHPLSPQGHPARLHRIVPRLRDVFGWGNLTCPICKGLFTAIN 140
|||||
49 RVLWAPAEAHPLSPQGHPARLHRIVPRLRDVFGWGNLTCPICKGLFTAIN 98
.
141 LGLKKEPNVARVGSVAIKLCNLLKIAPPAVCQSI VHLFEDDMVEVWRRSV 190
|||||
99 LGLKKEPNVARVGSVAIKLCNLLKIAPPAVCQSI VHLFEDDMVEVWRRSV 148
.
191 LSPSEACGLLLGSTCGHWDIFSSWNISLPTVPKPPKPPSPAPGAPVSR 240
|||||
149 LSPSEARGLLLGSTCGHWDIFSSWNISLPTVPKPPKPPSPAPGAPVSR 198
.
241 ILFLTDLHWDHDYLEGTDPCADPLCCRRGSLPPASRPGAGYWGEYSKC 290
|||||
199 ILFLTDLHWDHDYLEGTDPCADPLCCRRGSLPPASRPGAGYWGEYSKC 248

FIG. 2

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291 DLPLRTLESLLSGLGPAGPFDMVYWTGDI PAHDVWHQTRQDQLRALTTVT 340
|||||
249 DLPLRTLESLLSGLGPAGPFDMVYWTGDI PAHDVWHQTRQDQLRALTTVT 298
.
341 ALVRKFLGPVPVYPAVGNHES TPVNSFPFPFIEGNHSSRWLYEAMAKAWE 390
|||||
299 ALVRKFLGPVPVYPAVGNHES TPVNSFPFPFIEGNHSSRWLYEAMAKAWE 348
.
391 PWLP AEALRTL RIGGFYALSPY PGLRLISLNMNFC SRENFWLLINSTDPA 440
|||||
349 PWLP AEALRTL RIGGFYALSPY PGLRLISLNMNFC SRENFWLLINSTDPA 398
.
441 GQLQWL VGELQAAEDRGDKVHIIGHIPPGHCLKSWSNYYRIVARYENTL 490
|||||
399 GQLQWL VGELQAAEDRGDKVHIIGHIPPGHCLKSWSNYYRIVARYENTL 448
.
491 AAQFFGHTHVDEFVYDEETLSRPLAVAF LAPSATTYIGLNPLVSEAE G 540
|||||
449 AAQFFGHTHVDEFVYDEETLSRPLAVAF LAPSATTYIGLN P..... 491
.

FIG. 2 (CONT.¹)

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541 SLPYPGVGGIGEGGWSQSLQSMGRMCGPSLEIPLLLAPPVSPTSLAGYRV 590
      |||||
492 .....GYRV 495

      .
591 YQIDGNYSGSSHVVLDHETIILNLTQANIPGAIPHWQLLYRARETYGLPN 640
      |||||
496 YQIDGNYSGSSHVVLDHETIILNLTQANIPGAIPHWQLLYRARETYGLPN 545

      .
641 TLPTAWHNLVYRMRGDMQLFQTFWFLYHKGHPPEPCGTPCRLATLCAQL 690
      |||||
546 TLPTAWHNLVYRMRGDMQLFQTFWFLYHKGHPPEPCGTPCRLATLCAQL 595

      .
      691 SARADSPALCRHLMFPGSLPEAQSLWPRPLFC 722
      |||||
      596 SARADSPALCRHLMFPGSLPEAQSLWPRPLFC 627

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FIG. 2 (CONT.²)

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1 LLLGFLVLSLESTLSIPPWEAPKEHKYKAAEHTVVLTVTGEPCHFQY 50
  |||||
4 LLLGFLVLSLESTLSIPPWEAPKEHKYKAAEHTVVLTVTGEPCHFQY 53
  .
51 HRQLYHKCTHKGRPGPQWCATTPNFDQDQRWGYCLEPKKVKDCHSKHSP 100
  |||||
54 HRQLYHKCTHKGRPGPQWCATTPNFDQDQRWGYCLEPKKVKDCHSKHSP 103
  .
101 CQKGGTCVNMPSGPHCLCPQHLTGNNHCQKEKCFEPQLLRFHKNFIWYRT 150
  |||||
104 CQKGGTCVNMPSGPHCLCPQHLTGNNHCQKEKCFEPQLLRFHKNFIWYRT 153
  .
151 EQAAVARCQCKGPD AHCQRLASQACRTNPCLHGGRCLVEGHR LCHCPVG 200
  |||||
154 EQAAVARCQCKGPD AHCQRLASQACRTNPCLHGGRCLVEGHR LCHCPVG 203
  .
201 YTGPFCDVDTKASCYDGRGLSYRGLARTTL SGAPCQPWASEATYRNV TAE 250
  |||||
204 YTGPFCDVDTKASCYDGRGLSYRGLARTTL SGAPCQPWASEATYRNV TAE 253
  .

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FIG. 3

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251 QARNWGLGGHAFCRNPNDNIRPWCFVLNRDRLSWEYCDLAQCQTPTQAAAP 300
|||||
254 QARNWGLGGHAFCRNPNDNIRPWCFVLNRDRLSWEYCDLAQCQTPTQAAAP 303
|||||

301 PTPVSPRLHVPLMPAQAPPKPQPTTRTPPQSQTTPGALPAKREQPPSLTR 350
|||||
304 PTPVSPRLHVPLMPAQAPPKPQPTTRTPPQSQTTPGALPAKREQPPSLTR 353
|||||

351 NGPLSCGQRLRKSLSMTRVVGGLVALRGAHPYIAALYWGHSCAGSLIA 400
|||||
354 NGPLSCGQRLRKSLSMTRVVGGLVALRGAHPYIAALYWGHSCAGSLIA 403
|||||

401 PCWVLTAACHCLQDRPAPEDLTVVLGQERRNHSCEPCQTLAVRSYRLHEAF 450
|||||
404 PCWVLTAACHCLQDRPAPEDLTVVLGQERRNHSCEPCQTLAVRSYRLHEAF 453
|||||

451 SPVSYQHDLALLRLQEDADGSCALLSPYVQPVCLPSGAARPSETTLCQVA 500
|||||
454 SPVSYQHDLALLRLQEDADGSCALLSPYVQPVCLPSGAARPSETTLCQVA 503
|||||

501 GWGHQFEAS 509
|||||
504 GWGHQFEGA 512

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FIG. 3 (CONT.¹)

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1 MARLGNCSLTWAALIILLPGSLEECGHISVAPIVHLGDPITASCIKQ 50
  |||||
1 MARLGNCSLTWAALIILLPGSLEECGHISVAPIVHLGDPITASCIKQ 50

51 NCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLNHTQAFLS 100
  |||||
51 NCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLNHTQAFLS 100

101 CCLNWGNSLQILDQVELRAGYPPIAPHNLSCLMNLTSSLICQWEPGPET 150
  |||||
101 CCLNWGNSLQILDQVELRAGYPPIAPHNLSCLMNLTSSLICQWEPGPET 150

151 HLPTSFTLKSFRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNMG 200
  |||||
151 HLPTSFTLKSFRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNMG 200

201 IWVQAEALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPQAGCLQ 250
  |||||
201 IWVQAEALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPQAGCLQ 250

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FIG. 4

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251 LCWEPWQPGHLHINQKCELRHKPQGEASWALVGPLPLEALQYELCGLLPA 300
    |||||
251 LCWEPWQPGHLHINQKCELRHKPQGEASWALVGPLPLEALQYELCGLLPA 300

301 TAYTLQIRCIRWPLPGHWSL..... 320
    |||||
301 TAYTLQIRCIRWPLPGHWSLSPSLELRTTERTAPTVRDLTWWRQRQLDPR 350

321 .....GAILPLCNTTELSCTFHLP 339
    |||||
351 TVQLFWKPVLEEDSGRIQGYVVSWRPSGQAGAILPLCNTTELSCTFHLP 400

340 SEAQEVALVAYNSAGTSRPTPVVFESESRGPALTRLHAMARDPHSLWVGWE 389
    |||||
401 SEAQEVALVAYNSAGTSRPTPVVFESESRGPALTRLHAMARDPHSLWVGWE 450

390 PPNPWPQGYVIEWGLGPPSASNSNKTWRMEQNGRATGFLLENIRPFQLY 439
    |||||
451 PPNPWPQGYVIEWGLGPPSASNSNKTWRMEQNGRATGFLLENIRPFQLY 500

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FIG. 4 (CONT.¹)

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      . . . . .
690 LYGQLLGSPSPGPGHYLRCDSTQPLLAGLTPSPKSYENLWFQASPLGTL 739
      |||||
751 LYGQLLGSPSPGPGHYLRCDSTQPLLAGLTPSPKSYENLWFQASPLGTL 800
      . . . . .

      740 VTPAPSQEDDCVFGPLLNFPLLQGIIRVHGMEALGSF 775
          |||||
      801 VTPAPSQEDDCVFGPLLNFPLLQGIIRVHGMEALGSF 836

```

FIG. 4 (CONT. ³)

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```

MARLGNCSLTWAALIIILLPGSLEECGHISVSAPIVHLGDPITASCIKQ 50
|||||
1 MARLGNCSLTWAALIIILLPGSLEECGHISVSAPIVHLGDPITASCIKQ 50

51 NCSHLDPEPQILWRLGAELQPGGRQQRRLSDGTQESIITLPHLNHTQAFLS 100
|||||
51 NCSHLDPEPQILWRLGAELQPGGRQQRRLSDGTQESIITLPHLNHTQAFLS 100

101 CCLNWGNSLQILDQVELRAGYPPIPHNLSCLMNLTSSLICQWEPGPET 150
|||||
101 CCLNWGNSLQILDQVELRAGYPPIPHNLSCLMNLTSSLICQWEPGPET 150

151 HLPTSFTLKSFKSRGNCQTQGDSILDCVPKDQGQSHCCIPRKHLLLYQNMG 200
|||||
151 HLPTSFTLKSFKSRGNCQTQGDSILDCVPKDQGQSHCCIPRKHLLLYQNMG 200

201 IWVQAEALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPQAGCLQ 250
|||||
201 IWVQAEALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPQAGCLQ 250

```

FIG. 5

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```

. . . . .
501 EIIVTPLYQDTMGPSQHVYAYSQEMAPSHAPELHLKHIGKTWAQLEWVPE 550
|||||
501 EIIVTPLYQDTMGPSQHVYAYSQEMAPSHAPELHLKHIGKTWAQLEWVPE 550

. . . . .
551 PPELGKSPLTHYTI FWTNAQNQSFCEXLSSTAPEGLEGAQLPRRXFT 600
|||||
551 PPELGKSPLTHYTI FWTNAQNQSF..... 574

. . . . .
601 IQAYADRTPLPAAILNASSRGFVLHGLEPASLYHIHLMAASQAGATNSTV 650
. |||||
575 .....SAILNASSRGFVLHGLEPASLYHIHLMAASQAGATNSTV 613

. . . . .
651 LTLMTLTPEGSELHIIILGLFGLLLLTCLCGTAWLCCSPNRKNPLWPSVP 700
|||||
614 LTLMTLTPEGSELHIIILGLFGLLLLTCLCGTAWLCCSPNRKNPLWPSVP 663

. . . . .
701 DPAHSSLGSWVPTIMEEDAFQLPGLGTPPITKLTVLEEDEKPPVPWESHN 750
|||||
664 DPAHSSLGSWVPTIMEEDAFQLPGLGTPPITKLTVLEEDEKPPVPWESHN 713

```

FIG. 5 (CONT.²)

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```

7751 SSETCGLPTLVQTYVLQGDPRAVSTQPQSQSGTSDQVLYGQLLGSPTSPG 800
      |||||
7714 SSETCGLPTLVQTYVLQGDPRAVSTQPQSQSGTSDQVLYGQLLGSPTSPG 763
      |||||

8801 PGHYLRCDSTQPLLAGLTPSPKSYENLWFQASPLGTLVTPAPSQEDDCVF 850
      |||||
7764 PGHYLRCDSTQPLLAGLTPSPKSYENLWFQASPLGTLVTPAPSQEDDCVF 813
      |||||

      .
      851 GPLLNFPLLQGIRVHGMEALGSF 873
      |||||
      814 GPLLNFPLLQGIRVHGMEALGSF 836

```

FIG. 5 (CONT.'³)

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1 MQKIMHISVLLSPVLWGLIFGVSSNSIQIGGLFPRGADQEYSAFRVGMVQ 50
|||||
1 MQKIMHISVLLSPVLWGLIFGVSSNSIQIGGLFPRGADQEYSAFRVGMVQ 50
|||||
51 FSTSEFRLTPHIDNLEVANSFAVTNAFCQSFRGVYAIFGFYDKKSVNTI 100
|||||
51 FSTSEFRLTPHIDNLEVANSFAVTNAFCQSFRGVYAIFGFYDKKSVNTI 100
|||||
101 TSFCGTLHVSEFITPSFPTDGTTHPFVIQMRPDLKGALLSLIEYYQWDKFAY 150
|||||
101 TSFCGTLHVSEFITPSFPTDGTTHPFVIQMRPDLKGALLSLIEYYQWDKFAY 150
|||||
151 LYDSDRGLSTLQAVLDSAAEKKWQVTAINVGNINNDKKDEMYRSLFQDLE 200
|||||
151 LYDSDRGLSTLQAVLDSAAEKKWQVTAINVGNINNDKKDEMYRSLFQDLE 200
|||||
201 LKKERRVILDCERDKVNDIVDQVITIGKHVKGYHYIIANLEFTDGDLLKI 250
|||||
201 LKKERRVILDCERDKVNDIVDQVITIGKHVKGYHYIIANLEFTDGDLLKI 250

FIG. 6

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251 QFGANVSGFIQVDYDDSLVSKFIERWSTLEEKEYPGAHTTTIKYTSALT 300
|||||
251 QFGANVSGFIQVDYDDSLVSKFIERWSTLEEKEYPGAHTTTIKYTSALT 300
|||||
301 YDAVQVMTEAFRNLRKQRIEISRRGNAGDCLANPAVPWGQGVIEIERALKQ 350
|||||
301 YDAVQVMTEAFRNLRKQRIEISRRGNAGDCLANPAVPWGQGVIEIERALKQ 350
|||||
351 VQVEGLSGNIKFDQNGKRINYTIMELKTNGPRKIGYWSEVDKMMVVTLT 400
|||||
351 VQVEGLSGNIKFDQNGKRINYTIMELKTNGPRKIGYWSEVDKMMVVTLT 400
|||||
401 ELPSGNDTSGLENKTVVVVTTILESYPVMMKKNHEMLEGNERYEGYCVDLA 450
|||||
401 ELPSGNDTSGLENKTVVVVTTILESYPVMMKKNHEMLEGNERYEGYCVDLA 450
|||||

FIG. 6 (CONT.¹)

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451	AEIAKHCGFKYKLTIVGDGKYGARDADTKIWNGMVGELVYGKADIAIAPL	500
451	AEIAKHCGFKYKLTIVGDGKYGARDADTKIWNGMVGELVYGKADIAIAPL	500
501	TITLVREEVIDFSKPFMSLGISIMIKKPKQSKPGVFSFLDPLAYEIMCI	550
501	TITLVREEVIDFSKPFMSLGISIMIKKPKQSKPGVFSFLDPLAYEIMCI	550
551	VFAYIGVSVVFLVSRFSPYEWHTTEEFEDGRETQSSSESTNEFGIFNSLWF	600
551	VFAYIGVSVVFLVSRFSPYEWHTTEEFEDGRETQSSSESTNEFGIFNSLWF	600
601	SLGAFMRQGCDISPRSLSGRIVGGVWFFTLIIISSYTANLAAFLTVERM	650
601	SLGAFMRQGCDISPRSLSGRIVGGVWFFTLIIISSYTANLAAFLTVERM	650
651	VSPIESAEDLSKQTEIAYGTLDSGSTKEFFRRRSKIAVFDKMWTYMRSAP	700
651	VSPIESAEDLSKQTEIAYGTLDSGSTKEFFRRRSKIAVFDKMWTYMRSAP	700

FIG. 6 (CONT.)

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```

701 SVFVRTTAEGVARVRKSKGYAYLLESTMNEYIEQRKPCDTMKVGNLDS 750
|||||
701 SVFVRTTAEGVARVRKSKGYAYLLESTMNEYIEQRKPCDTMKVGNLDS 750

751 KGYGIATPKGSSSLGTPVNLAVLKLSEQGVLDKLNKWWYDKGEXG 795
|||||
751 KGYGIATPKGSSSLGTPVNLAVLKLSEQGVLDKLNKWWYDKGECG 795

```

FIG. 6 (CONT.³)

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```

1  MKSIYFVAGLFVMLVQGSWQRSLQDTEEKSRFSASQADPLSDPDQMNE 50
   |||||||
1  MKSIYFVAGLFVMLVQGSWQRSLQDTEEKSRFSASQADPLSDPDQMNE 50

51 KRHSQGTFTSDYSKYLDSTRRAQDFVQWLMNTKRNRRNNIAKRHDEFERHAE 100
   |||||||
51 KRHSQGTFTSDYSKYLDSTRRAQDFVQWLMNTKRNRRNNIAKRHDEFERHAE 100

101 GTFTSVI.....FPEEVAIVEELGRRHADGS 126
    ||||| :      |||||||
101 GTFTSDVSSYLEGQAAKEFIAWLVKGRGRDDFPEEVAIVEELGRRHADGS 150

127 FSDEMNTISDNLAARDFINWLIQTKITDRK 156
    |||||||
151 FSDEMNTILDNLAARDFINWLIQTKITDRK 180

```

FIG. 7

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6 SGTARKTLHFEISKEGSDLSVVERAEVWFLKVPKANRTRTKVTIRLFQQ 55
|||||
129 SGTARKTLHFEISKEGSDLSVVERAEVWFLKVPKANRTRTKVTIRLFQQ 178
56 QKHPQGS LDTGEEAEVGLKGERSELLSEKVVVDARKSTWHVFPVSSSIQ 105
|||||
179 QKHPQGS LDTGEEAEVGLKGERSELLSEKVVVDARKSTWHVFPVSSSIQ 228
106 RLDDQGS LDRVIAACEQCQESGASVLLGKKKKKEEGEGKKKGEGG 155
|||||
229 RLDDQGS LDRVIAACEQCQESGASVLLGKKKKKEEGEGKKKGEGG 278
156 AGADEEKEQSHRPFMLQARQSEDPHRRRRRRGLECDGKVNICKKQFFV 205
|||||
279 AGADEEKEQSHRPFMLQARQSEDPHRRRRRRGLECDGKVNICKKQFFV 328

FIG. 8

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206 SFKDIGNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSSTVINHYRM 255
|||||
329 SFKDIGNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSSTVINHYRM 378
256 RGHSPFANLKSCCVPTKLRPMSMLYYDDGQNI IKKDIQNMI VEECCGS 303
|||||
379 RGHSPFANLKSCCVPTKLRPMSMLYYDDGQNI IKKDIQNMI VEECCGS 426

FIG. 8 (CONT.¹)

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```

1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSS 50
  |||||
1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSS 50

51 ERIDKQIRYILDGISALRKETCNXSNMC.....EKDG 82
  |||||
51 ERIDKQIRYILDGISALRKETCNKSNMCESKEALAEENLNLPKMAEKDG 100

83 CFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVQMSTKVL 132
  |||||
101 CFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVQMSTKVL 150

133 IQFLQKKAKNLDAITTPDPPTNASLLTKLQAQNWQLQDMTTHLILRSFKE 182
  |||||
151 IQFLQKKAKNLDAITTPDPPTNASLLTKLQAQNWQLQDMTTHLILRSFKE 200

183 FLQSSLRALRQM 194
  |||||
201 FLQSSLRALRQM 212

```

FIG. 9

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```

1 MNSFST..... 6
  |||||
1 MNSFSAFGPVAFSLGLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSS 50
  .
7 .....TCNKSNMCESSKEALAENNLNLPKMAEKDG 36
  |||||
51 ERIDKQIRYILDGISAIRKETCNKSNMCESSKEALAENNLNLPKMAEKDG 100
  .
37 CFQSGFNEETCLVKIITGLLEFEVYLEYLNRFESSEEQARAVQMSTKVL 86
  |||||
101 CFQSGFNEETCLVKIITGLLEFEVYLEYLNRFESSEEQARAVQMSTKVL 150
  .
87 IQFLQKKAKNLDAITTPDPPTTNASLLTKLQAQNQWLQDMTTHLILRSFKE 136
  |||||
151 IQFLQKKAKNLDAITTPDPPTTNASLLTKLQAQNQWLQDMTTHLILRSFKE 200
  .
137 FLQSSLRALRQM 148
  |||||
201 FLQSSLRALRQM 212

```

FIG. 10

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```

1  MPRLFLHLLLEFCLLLNQFSRAVAACKWKDDVIKLCGRELVRAQIAICGMS 50
   |||||
1  MPRLFLHLLLEFCLLLNQFSRAVAACKWKDDVIKLCGRELVRAQIAICGMS 50
   |||||

51  TWSKRSLSQEDAPQTPRPVAAGDFIQTVSLGISPDGGKALRTGSCFTREF 100
   |||||
51  TWSKRSLSQEDAPQTPRPVA..... 70

101 LGALSKLVPFINKDTETIIIMLEFIANLPPELKAALSERQPSLPQLQQY 150
   .:|||||
71.... EIVPSFINKDTETIIIMLEFIANLPPELKAALSERQPSLPQLQQY 115
   .

151 VPALKDSSLLFEEFKKLIRNRQSEAADSNPSELKYLGLDTHSQKKRRPYV 200
   |||||.|||||
116 VPALKDSNLSFEEFKKLIRNRQSEAADSNPSELKYLGLDTHSQKKRRPYV 165
   .

201 ALFEKCCCLIGCTKRSLAKYC 220
   |||||
166 ALFEKCCCLIGCTKRSLAKYC 185

```

FIG. 11

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```

1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTARKLPRNFVVD 50
  |||||
1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTARKLPRNFVVD 50

      . . . . .
51 YYETSSLCSQPAVV...GKQVCADPSESWVQEVVYDLELN 87
  |||||
51 YYETSSLCSQPAVVFQTKRSKQVCADPSESWVQEVVYDLELN 92

```

FIG. 12

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```

1 MGLAWGLGVLFMLHVCGTNRIPESGGDNSVFDIFELTGAARKGSGRRLVK 50
  |||||
1 MGLAWGLGVLFMLHVCGTNRIPESGGDNSVFDIFELTGAARKGSGRRLVK 50

51 GPDSSPAFRIEDANLIPVPDDKFQDLVDVRAEKGFLLLASLRQMKT 100
  |||||
51 GPDSSPAFRIEDANLIPVPDDKFQDLVDVRAEKGFLLLASLRQMKT 100

101 RGTLLALERKDHSGQVFSVVSNGKAGTLDLSLTQVKQHVVSVEEALLAT 150
  |||||
101 RGTLLALERKDHSGQVFSVVSNGKAGTLDLSLTQVKQHVVSVEEALLAT 150

151 GQWKSITLHVQEDRAQLYIDCEKMENAEADVPIQSVFTRDLASIRLRIA 200
  |||||
151 GQWKSITLHVQEDRAQLYIDCEKMENAEADVPIQSVFTRDLASIRLRIA 200

201 KGGVNDNFQGVQLQNVRFVFGTTPEDILRNKGCSSSTSVLLTLDNNVVNGS 250
  |||||
201 KGGVNDNFQGVQLQNVRFVFGTTPEDILRNKGCSSSTSVLLTLDNNVVNGS 250

```

FIG. 13

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251	SPAIR	NYIGHKTKDLQAICGISCDELSSMVLELRGLRTIVTTLQDSIRK	300
251	SPAIR	NYIGHKTKDLQAICGISCDELSSMVLELRGLRTIVTTLQDSIRK	300
301	VTEEN	KELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKK	350
301	VTEEN	KELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKK	350
351	VSCPIM	PCSNATVPDGECCPRCWPSADSADGWSPWSEWTSCSTSCGNGIQ	400
351	VSCPIM	PCSNATVPDGECCPRCWPSADSADGWSPWSEWTSCSTSCGNGIQ	400
401	QGRSC	DSLNNRCEGSSVQTRTCHIQCEDKRFKQDGGWSHWSPWSSCSVT	450
401	QGRSC	DSLNNRCEGSSVQTRTCHIQCEDKRFKQDGGWSHWSPWSSCSVT	450
451	CGDGV	ITRILCNPSPPQMNGKPCGEARETKACKKDACPINGGWPWSP	500
451	CGDGV	ITRILCNPSPPQMNGKPCGEARETKACKKDACPINGGWPWSP	500

FIG. 13 (CONT.)¹

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```

501  WDICSVTCGGGVQKRSRLCENNPTPQFGGKDCVGDVTENQICNKQDCPIDG 550
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501  WDICSVTCGGGVQKRSRLCENNPTPQFGGKDCVGDVTENQICNKQDCPIDG 550

551  CLSNPCFAGVKCTSYPDGSWKCGACPPGYSNGIQCTDVDECKEVPDACE 600
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
551  CLSNPCFAGVKCTSYPDGSWKCGACPPGYSNGIQCTDVDECKEVPDACE 600

601  NHNGEHRCENTDPGYNCLPCPPRFTGSQPFQGGVEHATANKQVCKPRNPC 650
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
601  NHNGEHRCENTDPGYNCLPCPPRFTGSQPFQGGVEHATANKQVCKPRNPC 650

651  TDGTHDCNKNACNYLGHYSDPMYRCECKPGYAGNGIICGEDTDLDGWPN 700
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
651  TDGTHDCNKNACNYLGHYSDPMYRCECKPGYAGNGIICGEDTDLDGWPN 700

701  ENLVCVANATYHCKKDCNCPNLP 722
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
701  ENLVCVANATYHCKKDCNCPNLP 722

```

FIG. 13 (CONT.²)

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1 MGLAWGLGVFLMHVCGTNRIPESGGDNVFDIFELTGAARKSGRRLLVK 50
|||||
1 MGLAWGLGVFLMHVCGTNRIPESGGDNVFDIFELTGAARKSGRRLLVK 50

51 GPDSSPAFRIEDANLIPVPDDKFQDLVDAVRAEKGFLLASLRQMKKT 100
|||||
51 GPDSSPAFRIEDANLIPVPDDKFQDLVDAVRTEKGFLLASLRQMKKT 100

101 RGTLLALERKDHSGQVFSVVSNGKAGTLDLSLTQVGKQHVVSVEEALLAT 150
|||||
101 RGTLLALERKDHSGQVFSVVSNGKAGTLDLSLTQVGKQHVVSVEEALLAT 150

151 GQWKSITLQVQEDRAQLYIDCEKMENAEALDVPIQSVFTRDLASIALRIA 200
|||||
151 GQWKSITLQVQEDRAQLYIDCEKMENAEALDVPIQSVFTRDLASIALRIA 200

201 KGGVNDNFQGVQLQNVRFVFGTTPEDILRNKGCSSSTSVLLTLDNNVVNGS 250
|||||
201 KGGVNDNFQGVQLQNVRFVFGTTPEDILRNKGCSSSTSVLLTLDNNVVNGS 250

FIG. 14

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2251	SPAIR	NYIGHK	TKDLQA	ICGISC	DELSSM	VLELR	GLRTIV	TTLQ	DSIRK	300
2251	SPAIR	NYIGHK	TKDLQA	ICGISC	DELSSM	VLELR	GLRTIV	TTLQ	DSIRK	300
301	VTEEN	KELANE	LRRPPL	CYHN	GVQYRN	NEEWT	VDSC	TECH	CQNSVTICKK	350
301	VTEEN	KELANE	LRRPPL	CYHN	GVQYRN	NEEWT	VDSC	TECH	CQNSVTICKK	350
351	VSCPI	MPCSN	ATVPD	GECC	PRCW	PSADS	ADGW	SPSE	WTSCSTSCGNGIQ	400
351	VSCPI	MPCSN	ATVPD	GECC	PRCW	PSADS	ADGW	SPSE	WTSCSTSCGNGIQ	400
401	QGRS	CDSL	NNRCE	GSSVQ	TRTCH	IQECD	KRFK	QDGG	SHWSPWSSCSVT	450
401	QGRS	CDSL	NNRCE	GSSVQ	TRTCH	IQECD	KRFK	QDGG	SHWSPWSSCSVT	450
451	CGD	GVIT	TRIL	CNSP	SPQM	NGKPC	EGEARE	TKACK	KDACPINGGWPWSP	500
451	CGD	GVIT	TRIL	CNSP	SPQM	NGKPC	EGEARE	TKACK	KDACPINGGWPWSP	500

FIG. 14 (CONT.)¹

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```
501 WDICSVTCTGGGVQKR SRLC NNP TP Q F G K D C V G D V T E N Q I C N K Q D C P I   548  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
501 WDICSVTCTGGGVQKR SRLC NNP TP Q F G K D C V G D V T E N Q I C N K Q D C P I   548
```

FIG. 14 (CONT.²)

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1 MGLAWGLGVLFMLHVCGTNRIPESGGDNSVDFIFELTGAARKGSGRRLLVK 50
|||||
1 MGLAWGLGVLFMLHVCGTNRIPESGGDNSVDFIFELTGAARKGSGRRLLVK 50

51 GPDSSPAFRIEDANLIPVPDDKFQDLVDVRAEKGFLLLASLRQMKKT 100
|||||
51 GPDSSPAFRIEDANLIPVPDDKFQDLVDVRAEKGFLLLASLRQMKKT 100

101 RGTLLALERKDHSGQVFSVNSNGKAGTLDLSLTVQKQHVVSVVEEALLAT 150
|||||
101 RGTLLALERKDHSGQVFSVNSNGKAGTLDLSLTVQKQHVVSVVEEALLAT 150

151 GQWKSITLFEVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLASIALRIA 200
|||||
151 GQWKSITLFEVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLASIALRIA 200

201 KGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSSSTSVLLTLDNNVVNGS 250
|||||
201 KGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSSSTSVLLTLDNNVVNGS 250

FIG. 15

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251 SPAIRNYIGHKTKDLQAICIGISCDELSSMVLELRGLRTIVTTLQDSIRK 300
|||||
251 SPAIRNYIGHKTKDLQAICIGISCDELSSMVLELRGLRTIVTTLQDSIRK 300
|||||
301 VTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKK 350
|||||
301 VTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKK 350
|||||
351 VSCPIPCSNA TVPDGECPCRCWPSPDSADDDGWSPWSEWTSCSTSCGNGIQ 400
|||||
351 VSCPIPCSNA TVPDGECPCRCWPSPDSADDDGWSPWSEWTSCSTSCGNGIQ 400
|||||
401 QRGRSCDSLNNRCEGSSVQTRTCHI QECDKRFKQDGGWSHWPSSCSVT 450
|||||
401 QRGRSCDSLNNRCEGSSVQTRTCHI QECDKRFKQDGGWSHWPSSCSVT 450
|||||
451 CGDGVITRIRLCNSPSPQMNGKPCGEARETKACKKDACP 490
|||||
451 CGDGVITRIRLCNSPSPQMNGKPCGEARETKACKKDACP 490
|||||

FIG. 15 (CONT. ¹)

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1 MGLAWGLGVLFMLHVCCTNRIPESGGDNSVDFIFELTGAARKGSGRRLVK 50
|||||
1 MGLAWGLGVLFMLHVCCTNRIPESGGDNSVDFIFELTGAARKGSGRRLVK 50

51 GPDSSPAFRIEDANLIPVPDDKFQDLDVDAVRAEKGFLLASLRQMKKT 100
|||||
51 GPDSSPAFRIEDANLIPVPDDKFQDLDVDAVRTEKGFLLASLRQMKKT 100

101 RGTLLALERKDHSGQVFSVVSNGKAGTLDLSLTVQGKHVVSVVEEALLAT 150
|||||
101 RGTLLALERKDHSGQVFSVVSNGKAGTLDLSLTVQGKHVVSVVEEALLAT 150

151 GQWKSITLFVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLASIALRIA 200
|||||
151 GQWKSITLFVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLASIALRIA 200

201 KGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSSSTSVLLTLDNNVVNGS 250
|||||
201 KGGVNDNFQGVLQNVRFVFGTTPEDILRNKGCSSSTSVLLTLDNNVVNGS 250

FIG. 16

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```

      . . . . .
251 SPAIRNYIGHKTKDLQAICGISCELSSMVLELRGLRTIVTTLQDSIRK 300
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 SPAIRNYIGHKTKDLQAICGISCELSSMVLELRGLRTIVTTLQDSIRK 300

      . . . . .
301 VTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKK 350
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 VTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKK 350

      . . . . .
351 VSCPIMPCSNATVPDGECCPRCWPSDSADDDGWSFWSEWTSCSTSCGNGIQ 400
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 VSCPIMPCSNATVPDGECCPRCWPSDSADDDGWSFWSEWTSCSTSCGNGIQ 400

      . . . . .
401 QGRSCDSLNNRCEGSSVQTRTCHIÇECDKCRCKHLSLGTW 441
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
401 QGRSCDSLNNRCEGSSVQTRTCHIÇECDKCRFKQ...DGGW 438

```

FIG. 16 (CONT.¹)

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```

251 LAKTLVGVGASLGRVAAALTAMDKPLGRCVGHAEVEEALLCMDGAGPP 300
|||||
251 LAKTLVGVGASLGRVAAALTAMDKPLGRCVGHAEVEEALLCMDGAGPP 300
|||||
301 DLRDLVTTLGGALLWLSGHAGTQAQGAARVAAA..... 333
|||||
301 DLRDLVTTLGGALLWLSGHAGTQAQGAARVAAALDDGSALGRFERMLAAQ 350
.
.
.
.
334 ..RALQEALVLSDRAPFAAPSPFAELVLPQQ 363
|||||
451 QSRALQEALVLSDRAPFAAPLPFAELVLPQQ 482

```

FIG. 17 (CONT.)¹

```

1 MAALMTPGTGAPPAPGDFSGEGSQGLPDPSPPEPKQLPELIRMKRDGGRLS 50
  |||||
1 MAALMTPGTGAPPAPGDFSGEGSQGLPDPSPPEPKQLPELIRMKRDGGRLS 50

51 EADIRGFVAAVNGSAQGAQIGAMLMAIRLRGMDLEETSVLTQALAQSGQ 100
  |||||
51 EADIRGFVAAVNGSAQGAQIGAMLMAIRLRGMDLEETSVLTQALAQSGQ 100

101 QLEWPEAWRQQLVDKXSTGGVGDKVSLVLAPALAAACGCKVPMISGRGLGH 150
  |||||
101 QLEWPEAWRQQLVDKXSTGGVGDKVSLVLAPALAAACGCKVPMISGRGLGH 150

151 TGGTLDKLESIPGFNVIQSPEQMQLLDQAGCCIVGQSEQLVLPADGILYA 200
  |||||
151 TGGTLDKLESIPGFNVIQSPEQMQLLDQAGCCIVGQSEQLVLPADGILYA 200

201 ARDVTATVDSLPLIT.....G.....WRG.SQ..P.....R 223
  |||||
201 ARDVTATVDSLPLITASILSKKLVEGLSALVVDVKF.GGAAVFPNQEQAR 249
  .....
```

FIG. 18

```

224 .....A....RVAAALTAMDKPLGRVCVGHAVEEALLCMDGAGP 259
      |   ||||| ||||| ||||| ||||| ||||| ||||| |||||
250 ELAKTLVGASGLRVAAALTAMDKPLGRVCVGHAVEEALLCMDGAGP 299
      .
260 PDLRDLVTTLGGALLWLSGHAGTQAQGAARVAAALDDGSALGRFERMLAA 309
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 PDLRDLVTTLGGALLWLSGHAGTQAQGAARVAAALDDGSALGRFERMLAA 349
      .
310 QGVDPGLARALCSGSPAERRQLLPRAREQEELLAPADGTVELVRALPLAL 359
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
350 QGVDPGLARALCSGSPAERRQLLPRAREQEELLAPADGTVELVRALPLAL 399
      .
360 VLHELGAGRSRAGEPLRLGVGAELLDVDVGQRLLRRGTPWLVRVHRDGPALSG 409
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400 VLHELGAGRSRAGEPLRLGVGAELLDVDVGQRLLRRGTPWLVRVHRDGPALSG 449
      .
      410 PQSRALQEALVLSDRAPFAAPSFFAELVLPQQ 442
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
      450 PQSRALQEALVLSDRAPFAAPIPFPAELVLPQQ 482

```

FIG. 18 (CONT.¹)

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```

1 MAALMTPGTGAPPAPGDFSGEGSQGLPDPSPPEPKQLPELIRMKRDGGRLS 50
  |||||
1 MAALMTPGTGAPPAPGDFSGEGSQGLPDPSPPEPKQLPELIRMKRDGGRLS 50

51 EADIRGEVAAVNGSAQGAQIGAMLMAIRLRGMDLEETSVLTQALAQSGQ 100
  |||||
51 EADIRGEVAAVNGSAQGAQIGAMLMAIRLRGMDLEETSVLTQALAQSGQ 100

101 QLEWPEAWRQQQLVDKXSTGGVGDKVSLVLA?ALAAACGCKVPMISGRGLGH 150
  |||||
101 QLEWPEAWRQQQLVDKXSTGGVGDKVSLVLA?ALAAACGCKVPMISGRGLGH 150

151 TGGTLDKLESIPGFNVIOQSPEQM?VLLDQAGCCIVGQSEQLVPADGILYA 200
  |||||
151 TGGTLDKLESIPGFNVIOQSPEQM?VLLDQAGCCIVGQSEQLVPADGILYA 200

201 ARDVTATVDSLPLITG.....WRG.....SQPRA... 224
  |||||
201 ARDVTATVDSLPLITASILSKKLVEGLSALVVDVKFEGGA?VFPNQEQARE 250

```

FIG. 19

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```

225 .....RVAAALTAMDKPLGRCVGHAEVEEALLCMDGAGPP 260
      |||||||
251 LAKTLVGVSGLRLRVAAALTAMDKPLGRCVGHAEVEEALLCMDGAGPP 300
      .
261 DLRDLVTTLGGALLWLSGHAGTQAQGAARVAAA..... 293
      |||||||
301 DLRDLVTTLGGALLWLSGHAGTQAQGAARVAAALDDGSALGRFERMLAAQ 350
      .
      .
      .
294 ..RALQEALVLSDRAPFAAPSPFAELVLPQQ 323
      |||||||
451 QSRALQEALVLSDRAPFAAPLPFAELVLPQQ 482

```

FIG. 19 (CONT.¹)


```

1 MMDEEEVEVSLPRFKLEESYDMESVLRLNLGMTDAFELGKADFSGMSQTDL 50
  |||||
261 MMDEEEVEVSLPRFKLEESYDMESVLRLNLGMTDAFELGKADFSGMSQTDL 310
  |||||

      .          .          .
51 SLSKVHKSFEVNEEGTEAAAAATAAIMMRCARFVPRFCADHPFLFFIQ 100
  |||||
311 SLSKVHKSFEVNEEGTEAAAAATAAIMMRCARFVPRFCADHPFLFFIQ 360
  |||||

      .
101 HSKTNGILFCGRFSSP 116
    | |||||
361 HRKTNGILFCGRFSSP 376
```

FIG. 21

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```

251 EKFEVWTRLDMMDEEEV..... 267
    |||||
251 EKFEVWTRLDMMDEEEVSLPRFKLEESYDMESVLRNLGMTDAFELGKA 300

268 .....EEGTEAAAAATAAIMMRCARFVPRFC 293
    |||||
301 DFSGMSQTDLSLSKVVKHSFVEVNEEGTEAAAAATAAIMMRCARFVPRFC 350

294 ADHPFLFFIQHSKTNGILFCGRFSSP 319
    |||||
351 ADHPFLFFIQHRTKNGILFCGRFSSP 376

```

FIG. 22 (CONT.¹)

```
. . . . .
```

```
1 MDVLAEANGTFALNLLKTLGKDNSKNVFFSPMSMSCALAMVYMGA KGNTA 50  
| | | | |  
1 MDVLAEANGTFALNLLKTLGKDNSKNVFFSPMSMSCALAMVYMGA KGNTA 50  
  
. . . . .
```

```
51 AQMAQILSFNKSGGGDIHQGFQSLLTEVNKTGTQYLLR..... 89  
| | | | |  
51 AQMAQILSFNKSGGGDIHQGFQSLLTEVNKTGTQYLLRVANRLFGEKSC 100  
.  
.  
.
```

```
. . . . .
```

```
90 ..... ESYDMESVLRLNLGMTDAFELGKA 112  
| | | | |
```

```
251 EKFEWTRLDMMDEEEVEVSLPRFKLEESYDMESVLRLNLGMTDAFELGKA 300  
  
. . . . .
```

```
1113 DFSGMSQTDL SL SKVVHK SF EVNEEG TEAAAATAA IMMRCAR FVP RFC 162  
| | | | |  
301 DFSGMSQTDL SL SKVVHK SF EVNEEG TEAAAATAA IMMRCAR FVP RFC 350  
  
. . . . .
```

```
163 ADHPFLFFIQHSKTN GILFCGRFSSP 188  
| | | | |  
351 ADHPFLFFIOHRKTN GILFCGRFSSP 376
```

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FIG. 23

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```

1 MDVLAEANGTFALNLLKTLGKDNSKNVFFSPMSMSCALAMVYMGAKGNTA 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MDVLAEANGTFALNLLKTLGKDNSKNVFFSPMSMSCALAMVYMGAKGNTA 50

```

```
51 AQMAQ 55
- | | | |
51 AQMAQ 55
```

FIG. 24

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FIG. 25

[illegible]

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FIG. 28

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252 DLIQYNFGWY PESPICEGRRNRCPPPPVPLNSKIQPHSTTYRHGERVHI 301
|||||
251 DLIQYNFGWY PESPICEGRRNRCPPPPVPLNSKIQPHSTTYRHGERVHI 300
|||||
302 ECELNFVIQGS EELLCENGKWT EPPKCI EEKEKVACEQPPSVENGVAHPH 351
|||||
301 ECELNFVIQGS EELLCENGKWT EPPKCI EEKEKVACEQPPSVENGVAHPH 350
|||||
352 SEIYYS GDKVTYRCGGGYS LRGSS TITCNRGRWTL PPECVENIENCKPPP 401
|||||
351 SEIYYS GDKVTYRCGGGYS LRGSS TITCNRGRWTL PPECVENIENCKPPP 400
|||||
402 DIANGVVVDGLLASYTTGSSVEYRCNEY YLLKGSETSRCEQGAWSPPVC 451
|||||
401 DIANGVVVDGLLASYTTGSSVEYRCNEY YLLKGSETSRCEQGAWSPPVC 450
|||||
452 LEPCTIDVDHMNRN NIIQLKWKYEGKILHGDLIDFVCKQGYNLSPSIP LSE 501
|||||
451 LEPCTIDVDHMNRN NIIQLKWKYEGKILHGDLIDFVCKQGYNLSPSIP LSE 500
|||||

FIG. 29 (CONT.¹)

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502 ISAQCNRGDVRYPMCIKESKGMCASPPVIRNGDIVSSAARTYENGSSVE 551
|||||
501 ISAQCNRGDVRYPMCIKESKGMCASPPVIRNGDIVSSAARTYENGSSVE 550
552 YRCFDNHFLQGSQNVYCVDGVWTTTPPSCLEP 582
|||||
551 YRCFDNHFLQGSQNVYCVDGVWTTTPPSCLEP 581

FIG. 29 (CONT.²)

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```

1 MPWGRRPTWLLAFLLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50
  |||||
1 MPWGRRPTWLLAFLLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50

. . . . .
51 PAPFLVFSQGKKSISRI..... 66
  |||||
51 PAPFLVFSQGKKSISRIDPDGTDGTHHQQLVVDAGISADMDIHYKKERLYWVDV 100
.
.
.
.
67 ..... WAIPSVIRVNKRTGQNRVRLQGSMLKPSSLVVVHPLAKPGADP 109
  |||||
701 DHLWVSDWAIPSVIRVNKRTGQNRVRLQGSMLKPSSLVVVHPLAKPGADP 750

. . . . .
110 CLYRNGGCEHICQESLGTARCLCREGFVKAWDGKMCPLPQDYPILSGENAD 159
  |||||
751 CLYRNGGCEHICQESLGTARCLCREGFVKAWDGKMCPLPQDYPILSGENAD 800
.
.
.

```

FIG. 30

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160 LSKEVTSLSNSTQAEVPDDDDGTESSTLVAEIMVSGMNYEDDCPGGCGSH 209
|||||
801 LSKEVTSLSNSTQAEVPDDDDGTESSTLVAEIMVSGMNYEDDCPGGCGSH 850
|||||
210 ARCVSDGETAECQCLKGFARDGNLCSDIDECVLARSDCPSTSSRCINTEG 259
|||||
851 ARCVSDGETAECQCLKGFARDGNLCSDIDECVLARSDCPSTSSRCINTEG 900
|||||
260 GYVCRCEGYEGDGI SCFDIDECQGAHNCAENAACTNTEGGYNCTCAGR 309
|||||
901 GYVCRCEGYEGDGI SCFDIDECQGAHNCAENAACTNTEGGYNCTCAGR 950
|||||
310 PSSPGLSCPDDSTAPSLLEDGHHLDRNSYPGCPSSYDGYCLNGGVCMHIE 359
|||||
951 PSSPGRSCPDDSTAPSLLEDGHHLDRNSYPGCPSSYDGYCLNGGVCMHIE 1000
|||||
360 SLDSYTCNCVIGYSGDRCQTRDLRWELRHAGYGQKHDIMVVAVCMVALV 409
|||||
1001 SLDSYTCNCVIGYSGDRCQTRDLRWELRHAGYGQKHDIMVVAVCMVALV 1050
|||||

FIG. 30 (CONT.¹)

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```

1 MPWGRRPTWLLAFLLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50
  |||||
1 MPWGRRPTWLLAFLLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50
  . . . . .
51 PAPFLVFSQGKKSISRI..... 66
  |||||
51 PAPFLVFSQGKKSISRIDPDGTDGTHQQLVVDAGISADMDIHYKKERLYWVDV 100
  . . .
67 ..... WAIPSVIRVNKRTGQNRVRLQGSMLKPSLVLVHPLAKPGADP 109
  |||||
701 DHLWVSDWAIPSVIRVNKRTGQNRVRLQGSMLKPSLVLVHPLAKPGADP 750
  .
110 CLYRNGGCEHICQESLGTARCLCREGFVKAWDGKMCPLPDYPILSGENAD 159
  |||||
751 CLYRNGGCEHICQESLGTARCLCREGFVKAWDGKMCPLPDYPILSGENAD 800
  . . .

```

FIG. 31

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160 LSKEVTSLSNSTQAEVPDDDDGTESSTLVAEIMVSGMNYEDDCGPGGCGSH 209
|||||
801 LSKEVTSLSNSTQAEVPDDDDGTESSTLVAEIMVSGMNYEDDCGPGGCGSH 850
210 ARCVSDGETAECQCLKGFA RDGNLCS DIDE CVLARSDCPSTSSRCINTEG 259
|||||
851 ARCVSDGETAECQCLKGFA RDGNLCS DIDE CVLARSDCPSTSSRCINTEG 900
260 GYVCRCEGYEGDGISCFDIDECQ RGAHNCAENAACTNTEGGYNCTCAGR 309
|||||
901 GYVCRCEGYEGDGISCFDIDECQ RGAHNCAENAACTNTEGGYNCTCAGR 950
310 PSSPGLSCP DSTAPSL LGEDGHHLDRNSYPGCPSSYDGYCLNGGVCMHIE 359
|||||
951 PSSPGRSCP DSTAPSL LGEDGHHLDRNSYPGCPSSYDGYCLNGGVCMHIE
1000

FIG. 31 (CONT.¹)

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```

360 SLDSYTCNCVIGYSGDRCQT.....
      379
      ||||||||||||||||
1001 SLDSYTCNCVIGYSGDRCQTRDLRWELRHAGYGQKHDMVVAVCMVALV
      1050
      .
      .
      .
      .
380 .....PPSSDRGPQIEGNHLSYRYPVGPEKLSLQSANG 415
      ||||||||||||||||||||||||||||
1151 PHIDGMGTGQSCWIPPSSDRGPQIEGNHLSYRYPVGPEKLSLQSANG
      1200
      .
      416 SCHERAPDLPRQTEPVQ 432
      |||||||||||||.
      1201 SCHERAPDLPRQTEPVK 1217

```

FIG. 31 (CONT.²)

FIG. 32

```

1 MPWGRRPTWLLAFLV..... 17
  |||||
1 MPWGRRPTWLLAFLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50
.
.
.
18 .....SAECQCLKGFARDGNLCSDIDECVLARSDCPSTSSRCINTEG 59
  .|||
851 ARCVSDGETAECQCLKGFARDGNLCSDIDECVLARSDCPSTSSRCINTEG 900
.
.
60 GYVCRCEGYEGDGISCFDIDECQRGAHNCAENAACTNTEGGYNCTCAGR 109
  |||
901 GYVCRCEGYEGDGISCFDIDECQRGAHNCAENAACTNTEGGYNCTCAGR 950
.
.
110 PSSPGLSCPDSTAPSLLGEDGHHLDNRNSYPGCPSSYDGYCLNGGVCMHIE 159
  ||||
951 PSSPGRSCPDSTAPSLLGEDGHHLDNRNSYPGCPSSYDGYCLNGGVCMHIE 1000
.
.

```

FIG. 33

```

18 .....SAECQCLKGFARDGNLCSIDIECVLARSDCPSTSSRCINTEG 59
    .|||||
851 ARCVSDGETAECQCLKGFARDGNLCSIDIECVLARSDCPSTSSRCINTEG 900

    .
60 GYVCRCSGEYEGDGISCFDIDECQRGAHNCAENAACTNTEGGYNCTCAGR 109
    |||||
901 GYVCRCSGEYEGDGISCFDIDECQRGAHNCAENAACTNTEGGYNCTCAGR 950

    .
110 PSSPGLSCPDPSTAPSLLGEDGHHLDNRNSYPGCPSSYDGYCLNGGVCMHIE 159
    |||||
951 PSSPGRSCPDPSTAPSLLGEDGHHLDNRNSYPGCPSSYDGYCLNGGVCMHIE 1000

```

160 SLDSYTCNCVIGYSGDRCQTRDLRWELRHAGYGQKHDIMVVAVCMVALV 209
|||||
1001 SLDSYTCNCVIGYSGDRCQTRDLRWELRHAGYGQKHDIMVVAVCMVALV 1050
210 LLLGLMGWGTYYRTRKQLSNPPKNPCDEPSGVS SSGPDSSSGAAVASC 259
|||||
1051 LLLGLMGWGTYYRTRKQLSNPPKNPCDEPSGVS SSGPDSSSGAAVASC 1100
260 PQPWFVLEKHQDPKNGSLPADGTNGAVVDAGLSPSLQLGSHLTSWRQK 309
|||||
1101 PQPWFVLEKHQDPKNGSLPADGTNGAVVDAGLSPSLQLGSHLTSWRQK 1150
310 PHIDGMGTGQSCWIPPSSDRGPQIEGNHLSYRYPVGPEKLHSLQSANG 359
|||||
1151 PHIDGMGTGQSCWIPPSSDRGPQIEGNHLSYRYPVGPEKLHSLQSANG 1200
360 SCHERAPDLPRQTEPVQ 376
|||||
1201 SCHERAPDLPRQTEPVK 1217

FIG. 33 (CONT.¹)

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```

1  MPWGR..... 5
   |||||
1  MPWGRPTWLLAFLLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50

      .
      .
      .

6  ..... KAWDGKMCLPQDYPILSGENAD 27
   |||||
751 CLYRNGGCEHICQESLGTARCLCREGFVKAWDGKMCLPQDYPILSGENAD 800

      .
      .
      .

28 LSKEVTSLSNSTQAEVPDDDGTESTSLVAEIMVSGMNYEDDCGPGCGSH 77
   |||||
801 LSKEVTSLSNSTQAEVPDDDGTESTSLVAEIMVSGMNYEDDCGPGCGSH 850

      .
      .
      .

78 ARCVSDGETAECQCLKGFARDGNLCSIDIECVLARSDCPSTSSRCINTEG 127
   |||||
851 ARCVSDGETAECQCLKGFARDGNLCSIDIECVLARSDCPSTSSRCINTEG 900

```

FIG. 34

FIG. 34 (CONT.¹)

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378 PHIDGMGTGQSCWIPSSDRGPQIEGNSHLPSYRPVGPEKLHSLQSANG 427
 1151 PHIDGMGTGQSCWIPSSDRGPQIEGNSHLPSYRPVGPEKLHSLQSANG 1200

428 SCHERAPDLPRQTEPVQ 444
 1201 SCHERAPDLPRQTEPVK 1217

FIG. 34 (CONT.²)

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1 MFRELNEALELKDAHAATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVG 50
|||||
337 MFRELNEALELKDAHAATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVG 386

51 PDSD 54

||||

387 PDSD 390

FIG. 35

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1 MKYPVWPRYSASLQPVVDSRHLTVATLEERPFI VESPDPGTG GCV PNTV 50
|||||
382 MKYPVWPRYSASLQPVVDSRHLTVATLEERPFI VESPDPGTG GCV PNTV 431
51 PCRRQSNHTFSSG DVA PYTKLCKGFCIDILKKLARVVKFSYDLYLV TNG 100
|||||
432 PCRRQSNHTFSSG DVA PYTKLCKGFCIDILKKLARVVKFSYDLYLV TNG 481
101 KHGKRVRGVWNGMIGEVYK RADMAIGSLTINEERSEI VDFSVPFVETGI 150
|||||
482 KHGKRVRGVWNGMIGEVYK RADMAIGSLTINEERSEI VDFSVPFVETGI 531
151 SVMVAR SNGTVSPSAFLEPYSPAVWMMFVMCLTVVAITVFMFEYFSPVS 200
|||||
532 SVMVAR SNGTVSPSAFLEPYSPAVWMMFVMCLTVVAITVFMFEYFSPVS 581
201 YNQNLTRGKKSGGPAFTIGKSVLLWALVFNN SVPIENPRGTTSKIMVLV 250
|||||
582 YNQNLTRGKKSGGPAFTIGKSVLLWALVFNN SVPIENPRGTTSKIMVLV 631
.

FIG. 36

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251 WAFFAVIFLASYTANLAAFMIEQYIDTVSGLSDKKFQRPDQYPPFRFG 300
|||||
632 WAFFAVIFLASYTANLAAFMIEQYIDTVSGLSDKKFQRPDQYPPFRFG 681
301 TVPNGSTERNIRSRYRDMHMHVKNQSVEDALTSCLKMGKLDAFIYDAA 350
|||||
682 TVPNGSTERNIRSRYRDMHMHVKNQSVEDALTSCLKMGKLDAFIYDAA 731
351 VLNYMAGKDEGCKLVTIGSGKVFATTGYGIAQKDSHWKRAIDLALLQFL 400
|||||
732 VLNYMAGKDEGCKLVTIGSGKVFATTGYGIAQKDSHWKRAIDLALLQFL 781
401 GDGETQKLETVWLSGICQNEKNEVMSSKLDIDNMAGVFYMLLVAMGLALL 450
|||||
782 GDGETQKLETVWLSGICQNEKNEVMSSKLDIDNMAGVFYMLLVAMGLALL 831
451 VFAWEHLVYWKLRHSVPNSSQLDFLLAFSRGIYSCFSGVQSLASPPRQAS 500
|||||
832 VFAWEHLVYWKLRHSVPNSSQLDFLLAFSRGIYSCFSGVQSLASPPRQAS 881
.

FIG. 36 (CONT.¹)

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501 PDLTASSAQASVLKMLQAARDMVTTAGVSSSLDRATRTIENWGGRRAPP 550
|||||
882 PDLTASSAQASVLKMLQAARDMVTTAGVSSSLDRATRTIENWGGRRAPP 931
|||||
551 PSPCPTPRSGPSPCLPTPDRPPEPSPTGWGPPDGGRAALVRRAPQPPGRP 600
|||||
932 PSPCPTPRSGPSPCLPTPDRPPEPSPTGWGPPDGGRAALVRRAPQPPGRP 981
|||||
601 PTPGPPPLSDVSRVSRPPAWEARWPVRTGHCGRHLSASERPLSPARCHYSS 650
|||||
982 PTPGPPPLSDVSRVSRPPAWEARWPVRTGHCGRHLSASERPLSPARCHYSS 1031
|||||
651 FPRADRSGRPFLLFPPEPELEDPLLGPEQLARREALLHAAWARGSRPR 700
|||||
1032 FPRADRSGRPFLLF...PELEDPLLGKEQLARREALLHAAWARGSRPR 1078
|||||
701 HASLPSSVAEAFARPSSLPAGCTGPACARPDGHSACRRLAQAQSMCLPIY 750
|||||
1079 HASLPSSVAEAFARPSSLPAGCTGPACARPDGHSACRRLAQAQSMCLPIY 1128
|||||

FIG. 36 (CONT.²)

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```
751 REACQEGEQAGAPAWQHRQHVCLHAHAHL PFCWGAVCPHLPPCASHGSWL 800
    |||||||
1129 REACQEGEQAGAPAWQHRQHVCLHAHAHL PFCWGAVCPHLPPCASHGSWL 1178
    .
    .
801 SGAWGPLGHRGRTLGLGTGYRDSGGLDEISXVARGTQGFPGCTWRRISS 850
    |||||||
1179 SGAWGPLGHRGRTLGLGTGYRDSGGLDEISRARGTQGFPGCTWRRISS 1228
    .
    .
851 LESEV 855
    |||||
1229 LESEV 1233
```

FIG. 36 (CONT.³)

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1 MRLAVGALLVCAVLGLCLAVPDKTVRWCAVSEHEATKCQSFDRDHMKSVIP 50
|||||
1 MRLAVGALLVCAVLGLCLAVPDKTVRWCAVSEHEATKCQSFDRDHMKSVIP 50
|||||
51 SDGPSVACVKKASYLDCIRAIANEADAVTLDAGLVYDAYLAPNNLKPVV 100
|||||
51 SDGPSVACVKKASYLDCIRAIANEADAVTLDAGLVYDAYLAPNNLKPVV 100
|||||
101 AEFYGSKEDPQTFYYAVAVVKKDSGFQMNQLRGKKSCHTGLGRSAGWNIP 150
|||||
101 AEFYGSKEDPQTFYYAVAVVKKDSGFQMNQLRGKKSCHTGLGRSAGWNIP 150
|||||
151 IGLLYCDLPEPRKPLEKAVANFFSGSCAPCADGTDFFPQLCQLCPGCGCST 200
|||||
151 IGLLYCDLPEPRKPLEKAVANFFSGSCAPCADGTDFFPQLCQLCPGCGCST 200
|||||
201 LNQYFGYSGAFKCLKDGAGDVAFVKHSTIFENLANKADRQYELLCLDNT 250
|||||
201 LNQYFGYSGAFKCLKDGAGDVAFVKHSTIFENLANKADRQYELLCLDNT 250
|||||

FIG. 37

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251 RKPVDEYKDCHLAQVPSHTTVVARSMGGKEDLIWELLNQAQEHFGKDSKE 300
|||||
251 RKPVDEYKDCHLAQVPSHTTVVARSMGGKEDLIWELLNQAQEHFGKDSKE 300
|||||
301 FQFSSPHGKDLLFKDSAAGHFLKVPVRMDAKMYLGYEYVTAIRNLREGTC 350
|||||
301 FQFSSPHGKDLLFKDSAAGHFLKVPVRMDAKMYLGYEYVTAIRNLREGTC 350
|||||
351 PEPTDECKPVKWCALSHHERLKCDEWSVNSVGKIECVSAETTEDCIAKI 400
|||||
351 PEPTDECKPVKWCALSHHERLKCDEWSVNSVGKIECVSAETTEDCIAKI 400
|||||
401 MNGEADAMSLDGGFVYIAGKCGLVPVLAENYNKSDNCEDTPEAGYFAVAV 450
|||||
401 MNGEADAMSLDGGFVYIAGKCGLVPVLAENYNKSDNCEDTPEAGYFAVAV 450
|||||
451 VKKSASDLTWDNLKGKKKSCHTAFGRTAGWNIPMGLLYNKINHCRFDEFFS 500
|||||
451 VKKSASDLTWDNLKGKKKSCHTAFGRTAGWNIPMGLLYNKINHCRFDEFFS 500
|||||

FIG. 37 (CONT.¹)

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501 EGCA[.]PGSKKDSSLCKLCMGSGNLNCEPNNKEGYGYTGAFRC[.]LV[.]EKG[.]DVA 550
|||||
501 EGCA[.]PGSKKDSSLCKLCMGSGNLNCEPNNKEGYGYTGAFRC[.]LV[.]EKG[.]DVA 550
|||||
551 FVKHQ[.]TV[.]PPQNTGGKNPDPWAKNLNEKDYELLCLD[.]GTRK[.]PPVEEYANCH[.]LAR 600
|||||
551 FVKHQ[.]TV[.]PPQNTGGKNPDPWAKNLNEKDYELLCLD[.]GTRK[.]PPVEEYANCH[.]LAR 600
|||||
601 APNHAVVTRKDK[.]EACVHKILRQQ[.]HLFGSNVTD[.]CSGNFCLFRSETK[.]DLLF 650
|||||
601 APNHAVVTRKDK[.]EACVHKILRQQ[.]HLFGSNVTD[.]CSGNFCLFRSETK[.]DLLF 650
|||||
651 RDDT[.].....H.....LLEACT[.]FRRP 665
|||||
651 RDDTVCLAKLH[.]DRNTYEKYLGE[.]EYVKAVGNLRK[.]CS[.]TS[.]SS[.]LLEACT[.]FRRP 698
|||||

FIG. 37 (CONT.²)

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251 RKPVDEYKDCCHLAQVPSHTVVARSMGCKEDLIWELLNQAQEHFGKDKSKE 300
|||||
251 RKPVDEYKDCCHLAQVPSHTVVARSMGCKEDLIWELLNQAQEHFGKDKSKE 300
301 FQLFSSPHGKDLLFKDSAHGFLKVPPRMDAKMYLGYEYVTAIRNLREGTC 350
|||||
301 FQLFSSPHGKDLLFKDSAHGFLKVPPRMDAKMYLGYEYVTAIRNLREGTC 350
351 PEAPTDECKPVKWCALSHHERLKCDEWSVNSVGKIECVSAETTEDCIAKI 400
|||||
351 PEAPTDECKPVKWCALSHHERLKCDEWSVNSVGKIECVSAETTEDCIAKI 400
401 MNGEADAMSLDGGFVYIAGKCGLPVLAENYNKSDNCEDTPEAGYFA... 447
|||||
401 MNGEADAMSLDGGFVYIAGKCGLPVLAENYNKSDNCEDTPEAGYFAVAV 450
448E 448
451 VKKSASDLTWDNLKGKKKSCHTAVGRTAGWNIPMGLLYNKINHCRFDEFFS 500

FIG. 38 (CONT.¹)

```

449  EGCAPGSKDSSLCKLCMGSGNLNCEPNNKEGYYGYTGAFRCLVEKGDVA 498
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501  EGCAPGSKDSSLCKLCMGSGNLNCEPNNKEGYYGYTGAFRCLVEKGDVA 550
      . . . . . . . . . . . . . . . . . . . . . . . . . . . .

499  FVKHQTVPQNTGGKNPDWAKNLNEKDYELLCLDGTGRKPVVEEYANCHLAR 548
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
551  FVKHQTVPQNTGGKNPDWAKNLNEKDYELLCLDGTGRKPVVEEYANCHLAR 600
      . . . . . . . . . . . . . . . . . . . . . . . . . . . .

549  APNHAVVTRKDKEACVHKILRQQQHLFGSNVTD CSGNFCLFRSETKDLLF 598
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
601  APNHAVVTRKDKEACVHKILRQQQHLFGSNVTD CSGNFCLFRSETKDLLF 650
      . . . . . . . . . . . . . . . . . . . . . . . . . . . .

599  RDDTVCLAKLHDRNTYEKYLGE EYVKAVGNL RKCSTSSLLEACTFRRP 646
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
651  RDDTVCLAKLHDRNTYEKYLGE EYVKAVGNL RKCSTSSLLEACTFRRP 698

```

FIG. 38 (CONT. 2)

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1 MAEGEGGEDEIQFLRTEDEVVLQCIATIHKEQKFCCLAAEGLGNRLCFL 50
|||||
1 MAEGEGGEDEIQFLRTEDEVVLQCIATIHKEQKFCCLAAEGLGNRLCFL 50

51 EPTSEAKYIPPDLCVCNFFVLEQSLSVRALQEMLAN TGENGEGGEGAAQGGH 100
|||||
51 EPTSEAKYIPPDLCVCNFFVLEQSLSVRALQEMLAN TGENGEGGEGAAQGGH 100

101 RTLLYGHAVLLRHHSFSGMYLTCLTTSRSQTDKLA FDVGLREHATGEACWW
|||||
101 RTLLYGHAVLLRHHSFSGMYLTCLTTSRSQTDKLA FDVGLREHATGEACWW 150

151 TIHPASKQRSEGEKVRIGDDLILVSVSSERYLHLSV SNNGNIQVDASFMT 200
|||||
151 TIHPASKQRSEGEKVRIGDDLILVSVSSERYLHLSV SNNGNIQVDASFMT 200

201 LWNVHPTCSGSSIEEGYLLGGHVVRFLFHGHDECLT IPSTDQND SQHRRIF 250
|||||
201 LWNVHPTCSGSSIEEGYLLGGHVVRFLFHGHDECLT IPSTDQND SQHRRIF 250

FIG. 39

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```

501 FAGIAREESGMWKEILNLLYKLLAALIRGNRNCAQFSNNLDWLISKLD 550
|||||
501 FAGIAREESGMWKEILNLLYKLLAALIRGNRNCAQFSNNLDWLISKLD 550

551 RLESSSGILEVLHCILTESPEALNLI AEGHIKSIISLLDKHGRNHKVLDI 600
|||||
551 RLESSSGILEVLHCILTESPEALNLI AEGHIKSIISLLDKHGRNHKVLDI 600

601 LCSLCLCNGVAVRANQNLCNLLPRRNLLQTRLINDVTSIRPNIFLGV 650
|||||
601 LCSLCLCNGVAVRANQNLCNLLPRRNLLQTRLINDVTSIRPNIFLGV 650

651 AEGSAQYKKWYFELIIDQVDPFLTAEPHLRVGWASSSGYAPXPGGEGW 700
|||||
651 AEGSAQYKKWYFELIIDQVDPFLTAEPHLRVGWASSSGYAPYPGGEGW 700

701 GGNGVGDDLYSYGFDGLHLWSGRIPRAVASXNQHLRSDDVVSCCL.DLG 749
|||||
701 GGNGVGDDLYSYGFDGLHLWSGRIPRAVASINQHLLRSDDVGKLLPGPRG 750

```

FIG. 39 (CONT.²)

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750 CPASHSASMGSPCRGCLRNFN TDGLFFPVMFSAGVKVRFLMGGRHGEFK 799
|||||
751 CPASHSASMGSPCRGCLRNFN TDGLFFPVMFSAGVKVRFLMGGRHGEFK 800
|||||
800 FLPPSGYAPCYEALLPKEKMRLEPVKEYKRDADGIRDLLGTTQFLSQASF 849
|||||
801 FLPPSGYAPCYEALLPKEKMRLEPVKEYKRDADGIRDLLGTTQFLSQASF 850
|||||
850 IPCPVDTSQVILPPHLEKIRDRLAENIHELWGMNKIELGWTFGKIRDDNK 899
|||||
851 IPCPVDTSQVILPPHLEKIRDRLAENIHELWGMNKIELGWTFGKIRDDNK 900
|||||
900 RQHPCLVEFSKLPETEKNYNLQMSTETLKTLLXLGCHIAHVNPAAEEDLK 949
|||||
901 RQHPCLVEFSKLPETEKNYNLQMSTETLKTLLXLGCHIAHVNPAAEEDLK 950
|||||
950 KVKLPKNYMSNGYKPAPLDLSDVKLLPPQEILVDKLAENAHNVWAKDRI 999
|||||
951 KVKLPKNYMSNGYKPAPLDLSDVKLLPPQEILVDKLAENAHNVWAKDRI 1000

FIG. 39 (CONT. ³)

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1000 KQGWYGIQQDLKNKRNPRLPYALLDERTKKNRDSLREAVRTFVGYG 1049
|||||
1001 KQGWYGIQQDLKNKRNPRLPYALLDERTKKNRDSLREAVRTFVGYG 1050
|||||
1050 NIEPSDQELADSAVEKVSIDKIRFFRVERSXXVRSWKWYFEFEVVTGGDM 1099
|||||
1051 NIEPSDQELADSAVEKVSIDKIRFFRVERSYPVRSWKWYFEFEVVTGGDM 1100
|||||
1100 RVGWARPGCRPDVELGADDQAFVFEGRGQRWHQSGYFGRTWQPGDVVG 1149
|||||
1101 RVGWARPGCRPDVELGADDQAFVFEGRGQRWHQSGYFGRTWQPGDVVG 1150
|||||
1150 CMINLDDASMIFTLNGELLITNKGSELAFAADYEIENGFPICCLGLSQIG 1199
|||||
1151 CMINLDDASMIFTLNGELLITNKGSELAFAADYEIENGFPICCLGLSQIG 1200
|||||
1200 RMNLGTDASTEKFYTMCGLQEGEFPFAVNMNRDVAMWFSKRLPTFVNVPK 1249
|||||
1201 RMNLGTDASTEKFYTMCGLQEGEFPFAVNMNRDVAMWFSKRLPTFVNVPK 1250

FIG. 39 (CONT.⁴)

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1250	DPHIEVMRIDGTMDSP	CLKVTHKTFGTQNS	ADMIYCRLSMP	VECHSS	1299
1251	DPHIEVMRIDGTMDSP	CLKVTHKTFGTQNS	ADMIYCRLSMP	VECHSS	1300
	
1300	FSHSPCLDSEAFQKRKQ	MEILSHTTTQCY	YAIRIFXGQD	PSCVWVGWVT	1349
1301	FSHSPCLDSEAFQKRKQ	MEILSHTTTQCY	YAIRIFGQD	PSCVWVGWVT	1350
	
1350	PDYHLYSEKFDLNKNCT	VTVTLGDERGRV	HESVKRSNCY	MVWGGDIVASS	1399
1351	PDYHLYSEKFDLNKNCT	VTVTLGDERGRV	HESVKRSNCY	MVWGGDIVASS	1400
	
1400	QRSNRSNVDLEIGCLVD	LAMGMLSF	SANGKELGTCYQ	VEPNTKVFPAVFL	1449
1401	QRSNRSNVDLEIGCLVD	LAMGMLSF	SANGKELGTCYQ	VEPNTKVFPAVFL	1450
	
1450	QPTSTSLFQFELGKLKN	AMPLSAAIFRSEEX	NPVFQCP	PRLDVQTIQPV	1499
1451	QPTSTSLFQFELGKLKN	AMPLSAAIFRSEEX	NPVFQCP	PRLDVQTIQPV	1500

FIG. 39 (CONT.⁵)

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11500	WSRMPNSFLK	VETERV	SERHGWV	VQCLEPLQ	MMALHI	PEENRCV	DILELC	1549
11501	WSRMPNSFLK	VETERV	SERHGWV	VQCLEPLQ	MMALHI	PEENRCV	DILELC	1550
	
11550	EQEDLMRFHY	HTLRYS	AVCALG	NSRVAY	ALCSHV	DLSQLFY	AIDNKYLP	1599
11551	EQEDLMRFHY	HTLRYS	AVCALG	NSRVAY	ALCSHV	DLSQLFY	AIDNKYLP	1600
	
11600	GLLRSGFYD	LLISIH	LASAK	ERKLM	MKNEYI	IPITST	TRNICLFP	1649
11601	GLLRSGFYD	LLISIH	LASAK	ERKLM	MKNEYI	IPITST	TRNICLFP	1650
	
11650	HGLPGVGL	RTCLKP	GFRFST	PCFVVT	GEDH	QKQSP	EIPLES	1699
11651	HGLPGVGL	RTCLKP	GFRFST	PCFVVT	GEDH	QKQSP	EIPLES	1700

FIG. 39 (CONT.)⁶

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1700 TEAVQCSGAHIRDPVGGSVFQFVPLKLTLLVMGVFDDDDVRQILL 1749
|||||
1701 TEAVQCSGAHIRDPVGGSVFQFVPLKLTLLVMGVFDDDDVRQILL 1750
|||||
1750 IDPSVFGEHSAGTEEGAEKEEVTQVEEKAVEAGEKAGKEAPVKGLLQTRL 1799
|||||
1751 IDPSVFGEHSAGTEEGAEKEEVTQVEEKAVEAGEKAGKEAPVKGLLQTRL 1800
|||||
1800 PESVKLQMCCELLSYLDCCELQHRVEAIVAFGDIYVSKLQANQKFRYNELM 1849
|||||
1801 PESVKLQMCCELLSYLDCCELQHRVEAIVAFGDIYVSKLQANQKFRYNELM 1850
|||||
1850 QALNMSAALTARKTKEFRSPPEQINMLLNFLQGENCPCPEEIREELYDF 1899
|||||
1851 QALNMSAALTARKTKEFRSPPEQINMLLNFLQGENCPCPEEIREELYDF 1900
|||||
1900 HEDLLHCGVPLEEEEEEDTSWTGKLCALVYKIKGPPKPEKEQPTTEE 1949
|||||
1901 HEDLLHCGVPLEEEEEEDTSWTGKLCALVYKIKGPPKPEKEQPTTEE 1950

FIG. 39 (CONT.)

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1950 ERCPTTLKELISQTMICWAQEDQIQDSELVRMMFNLLRRQYDSIGELLQA 1999
|||||
1951 ERCPTTLKELISQTMICWAQEDQIQDSELVRMMFNLLRRQYDSIGELLQA 2000
|||||
2000 LRKTYTISHTSVSDTINLLAALGQIRSLLSVRMGKEEELLMINGLDIMN 2049
|||||
2001 LRKTYTISHTSVSDTINLLAALGQIRSLLSVRMGKEEELLMINGLDIMN 2050
|||||
2050 NKVIFYQHPNLMRVLGMHETVMEVMNVNLGTEKSQIAFPKMVASCCRFLCY 2099
|||||
2051 NKVIFYQHPNLMRVLGMHETVMEVMNVNLGTEKSQIAFPKMVASCCRFLCY 2100
|||||
2100 FCRISRQNKAMFEHLSYLLENSSVGLASPSMRGSTPLDVAASSVMDNNE 2149
|||||
2101 FCRISRQNKAMFEHLSYLLENSSVGLASPSMRGSTPLDVAASSVMDNNE 2150
|||||
2150 LALSLEEPDLEKVVTYLAGCGLQSCPMLLAKGYPDVGNWPIEGERYLSFL 2199
|||||
2151 LALSLEEPDLEKVVTYLAGCGLQSCPMLLAKGYPDVGNWPIEGERYLSFL 2200

FIG. 39 (CONT.⁸)

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2200 RFAVFNSESEENASVVVKLLIRRPECFGPALRGEGGNGLAAMQGAIK 2249
|||||
2201 RFAVFNSESEENASVVVKLLIRRPECFGPALRGEGGNGLAAMQGAIK 2250
|||||
2250 ISENPALDLP SQGKREVSTEDDEEEEEIVHMGNAIMSFYSALIDLLGRC 2299
|||||
2251 ISENPALDLP SQGKREVSTEDDEEEEEIVHMGNAIMSFYSALIDLLGRC 2300
|||||
2300 APEMHLIQTGKGEAIRIRSILRSLVPTEDLVGIIISIPKLPSLNKDGVS 2349
|||||
2301 APEMHLIQTGKGEAIRIRSILRSLVPTEDLVGIIISIPKLPSLNKDGVS 2350
|||||
2350 EPDMAXNFCPDH KAPMVLF LDRVYGIKDQTFLLH LLEVGF L PDLRASASL 2399
|||||
2351 EPDMAGNFCPDH KAPMVLF LDRVYGIKDQTFLLH LLEVGF L PDLRASASL 2400
|||||
2400 DTVSLSTTEAALNRYICSAVLP LLTRCAPLFXGTEHCTSLIDSTLQTI 2449
|||||
2401 DTVSLSTTEAALNRYICSAVLP LLTRCAPLFGGTEHCTSLIDSTLQTI 2450

FIG. 39 (CONT.⁹)

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2450 YRLSKGRSLTKAQRDTIEECLLAICNHLRPSMLQQLLRRLVFDVDPQLNEY 2499
|||||
2451 YRLSKGRSLTKAQRDTIEECLLAICNHLRPSMLQQLLRRLVFDVDPQLNEY 2500
|||||
2500 CKMPLKLLTNHYYEQCWKYCYCLPSGWGSYGLAVEEELHLTEKLFWGI XDSL 2549
|||||
2501 CKMPLKLLTNHYYEQCWKYCYCLPSGWGSYGLAVEEELHLTEKLFWGI IDSL 2550
|||||
2550 SHKKYDPDLFRMALPCLSAIAGALPPDYLDXRITATLEKQISVDADGNFD 2599
|||||
2551 SHKKYDPDLFRMALPCLSAIAGALPPDYLDXSRITATLEKQISVDADGNFD 2600
|||||
2600 PKPINTMNFSLPEKLEYIVTKYAEHSHDKWACDKSQSGWKYGISLDENVK 2649
|||||
2601 PKPINTMNFSLPEKLEYIVTKYAEHSHDKWACDKSQSGWKYGISLDENVK 2650
|||||
2650 THPLIRPFKTLTEKEKEIYRWPAEESLKTMLAVGWTVERTKEGEALVQQR 2699
|||||
2651 THPLIRPFKTLTEKEKEIYRWPAEESLKTMLAVGWTVERTKEGEALVQQR 2700

FIG. 39 (CONT.¹⁰)

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2700 ENEKLRVSQANQNSYSPAPLDLSNVVLSRELQGMVEVVAENYHNIWAK 2749
|||||
2701 ENEKLRVSQANQNSYSPAPLDLSNVVLSRELQGMVEVVAENYHNIWAK 2750
|||||
2750 KKKLELESKGGSHPLLVPYDTLTAKEKFKDREKAQDLFKFLQVNGIIVS 2799
|||||
2751 KKKLELESKGGSHPLLVPYDTLTAKEKFKDREKAQDLFKFLQVNGIIVS 2800
|||||
2800 RGMKDMELDASSMEKRFXKFLKKILKYVDSAQEFIAHLEAIVSSGKTEK 2849
|||||
2801 RGMKDMELDASSMEKRFGYKFLKKILKYVDSAQEFIAHLEAIVSSGKTEK 2850
|||||
2850 SPRDQEIKFFAKVLLPLVDQYFTSHCLYFLSSPLKPLSSSGYASHKEKEM 2899
|||||
2851 SPRDQEIKFFAKVLLPLVDQYFTSHCLYFLSSPLKPLSSSGYASHKEKEM 2900
|||||
2900 VAGLFCKLAALVRHRISLFGSDSTTMVSLCHILAQTLDTRTVMKSGSELV 2949
|||||
2901 VAGLFCKLAALVRHRISLFGSDSTTMVSLCHILAQTLDTRTVMKSGSELV 2950

FIG. 39 (CONT.¹¹)

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2950 KAGLRAFFENAAEDLEKTS[.]ENLKL[.]GKFTHSR[.]TQIKGVSQNIN[.]YTTVALLP 2999
|||||
2951 KAGLRAFFENAAEDLEKTS[.]ENLKL[.]GKFTHSR[.]TQIKGVSQNIN[.]YTTVALLP 3000
|||||
3000 ILTSIFEHV[.]TQH[.]QFGMDLL[.]LGDVQ[.]ISCYHILCSLYSLGTGKNIYVERQ[.]RP 3049
|||||
3001 ILTSIFEHV[.]TQH[.]QFGMDLL[.]LGDVQ[.]ISCYHILCSLYSLGTGKNIYVERQ[.]RP 3050
|||||
3050 ALGEC[.]LASLAAAI[.]PVAFLEPTLNRYNPLSVFNTKTPRERSILGMPD[.]TVED 3099
|||||
3051 ALGEC[.]LASLAAAI[.]PVAFLEPTLNRYNPLSVFNTKTPRERSILGMPD[.]TVED 3100
|||||
3100 MCPDIPQ[.]LEGLMKEINDLAESGARYTEMPHVIEVILPMLCN[.]YLSYWWERG 3149
|||||
3101 MCPDIPQ[.]LEGLMKEINDLAESGARYTEMPHVIEVILPMLCN[.]YLSYWWERG 3150
|||||
3150 PENLPPSTG[.]PCCTKVTSEHLSLILGNILKIINN[.]NLGIDEASWMKRIAVYA 3199
|||||
3151 PENLPPSTG[.]PCCTKVTSEHLSLILGNILKIINN[.]NLGIDEASWMKRIAVYA 3200
|||||

FIG. 39 (CONT.¹²)

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3450 SAAVFHLEQVEQLRSKKAVWHKLLSKQRKRAVVACFRMAPLYNLPRHRS 3499
|||||
3451 SAAVFHLEQVEQLRSKKAVWHKLLSKQRKRAVVACFRMAPLYNLPRHRS 3500
|||||
3500 INFLHGYQRFWIEETEYSFEEKLVQDLAKSPKVEEEEEETEKQPDPLH 3549
|||||
3501 INFLHGYQRFWIEETEYSFEEKLVQDLAKSPKVEEEEEETEKQPDPLH 3550
|||||
3550 QIILYFSRNALTERSKLEDDPLYTSYSSMMAKSCQSGEDEDEDKEKTF 3599
|||||
3551 QIILYFSRNALTERSKLEDDPLYTSYSSMMAKSCQSGEDEDEDKEKTF 3600
|||||
3600 EEKEMEKOQKTLYQQARLHERGAAEMVLQMISSASKGEMSPMVVETLKLGLIA 3649
|||||
3601 EEKEMEKOQKTLYQQARLHERGAAEMVLQMISSASKGEMSPMVVETLKLGLIA 3650
|||||
3650 ILNGGNAGVQQKMLDYLKEKKDAGFFQSLXGLMQSCSVLDLNAXERQNK 3699
|||||
3651 ILNGGNAGVQQKMLDYLKEKKDAGFFQSLPGLMQSCSVLDLNASERQNK 3700

FIG. 39 (CONT.¹⁴)

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3700 EGLGMVTEEGTLIVREGEKVLQNDDEFTRDLFRFLQLLCEGHN SDFQNFL 3749
|||||
3701 EGLGMVTEEGTLIVREGEKVLQNDDEFTRDLFRFLQLLCEGHN SDFQNFL 3750
|||||
3750 RTQMGNTTTVNVIISTVDYLLRLQESISDFYWYYSGKDIIDESGQHNF SK 3799
|||||
3751 RTQMGNTTTVNVIISTVDYLLRLQESISDFYWYYSGKDIIDESGQHNF SK 3800
|||||
3800 ALAVTKQIFNSLTEYIQGPCIGNQQSLAHSRLWDVAVGFLHVFANMQMKL 3849
|||||
3801 ALAVTKQIFNSLTEYIQGPCIGNQQSLAHSRLWDVAVGFLHVFANMQMKL 3850
|||||
3850 SQDSSQIELLKELLDLLQDMVVMLLSLLEGNVVNGTIGKQMVD TLVESST 3899
|||||
3851 SQDSSQIELLKELLDLLQDMVVMLLSLLEGNVVNGTIGKQMVD TLVESST 3900
|||||
3900 NVEMILKFFDMFLKLDLTSSDTFKEYDPDGKGIISKKEFQKAMEGQKQY 3949
|||||
3901 NVEMILKFFDMFLKLDLTSSDTFKEYDPDGKGIISKKEFQKAMEGQKQY 3950

FIG. 39 (CONT.¹⁵)

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3950 TQSEIDFLSCAEADENDMFNYVDFVDRFHEPAKDIGENVAVLLTNLSEH 3999
|||||
3951 TQSEIDFLSCAEADENDMFNYVDFVDRFHEPAKDIGENVAVLLTNLSEH 4000
|||||
4000 MPNDSRLKCLLDPAESVLNYFXPYLGRIEIMGGAKKIERVYFEISESRT 4049
|||||
4001 MPNDSRLKCLLDPAESVLNYFGPYLGRIEIMGGAKKIERVYFEISESRT 4050
|||||
4050 QWEKPQVKESKRQFIFDVVNEGGEQKMXL FVNFCEDTIFEMQLASQISE 4099
|||||
4051 QWEKPQVKESKRQFIFDVVNEGGEQKMG L FVNFCEDTIFEMQLASQISE 4100
|||||
4100 SDSADRPEEEEEDEDSYVLEIAGEEEEEEDGSLEPASAFAMACASVKRNV 4149
|||||
4101 SDSADRPEEEEEDEDSYVLEIAGEEEEEEDGSLEPASAFAMACASVKRNV 4150
|||||
4150 DFLKRATLKNLRKQYRNVKKMTAKELVKVLFSEFFWMLFVGLFQLLFTILG 4199
|||||
4151 DFLKRATLKNLRKQYRNVKKMTAKELVKVLFSEFFWMLFVGLFQLLFTILG 4200
|||||

FIG. 39 (CONT.¹⁶)

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4200 GIFQILWSTVFGGGLVEGAKNIRVTKILGDMPTQFGIHDDTMEAEAE 4249
|||||
4201 GIFQILWSTVFGGGLVEGAKNIRVTKILGDMPTQFGIHDDTMEAEAE 4250
|||||
4250 VMEPGITTELTVHFVFIKGEKGDTDIMSDLFGLHPKKEGSLKHGPEVGLGDLS 4299
|||||
4251 VMEPGITTELTVHFVFIKGEKGDTDIMSDLFGLHPKKEGSLKHGPEVGLGDLS 4300
|||||
4300 EIIIGKDEPPPLESTVQKKRKAQAEMKAANEAEKGKVESEKADMEDGEKED 4349
|||||
4301 EIIIGKDEPPPLESTVQKKRKAQAEMKAANEAEKGKVESEKADMEDGEKED 4350
|||||
4350 KDKEEEQAEYLWTEVTKKKKRRRCGQKVEKPEAFTANFFKGLEIYQTKLLH 4399
|||||
4351 KDKEEEQAEYLWTEVTKKKKRRRCGQKVEKPEAFTANFFKGLEIYQTKLLH 4400
|||||
4400 YLARNFYNLRFALFVAFAINFILLFYKVTEEPLEEEETEDVANLWNSFND 4449
|||||
4401 YLARNFYNLRFALFVAFAINFILLFYKVTEEPLEEEETEDVANLWNSFND 4450

FIG. 39 (CONT.¹⁷)

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4700 PDMKCDDMMTCYLFHMYVGVRRAGGGIGDEIEDPAGDPYEMYRIVFDITFF 4749
|||||
4701 PDMKCDDMMTCYLFHMYVGVRRAGGGIGDEIEDPAGDPYEMYRIVFDITFF 4750
|||||
4750 FFVIVILLAIQGLIIDAFAFGELRDQQEQVREDME 4783
|||||
4751 FFVIVILLAIQGLIIDAFAFGELRDQQEQVREDME 4784

FIG. 39 (CONT.¹⁹)

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```
251 LPTVCIGAWTAARLYLEDTCGWDNDHSDVPWWVIRIPILISIIVNFVLEI 300
|||||
251 LPTVCIGAWTAARLYLEDTCGWDNDHSDVPWWVIRIPILISIIVNFVLEI 300

301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPIS 350
|||||
301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLIPLFGVHYMVFAVFPIS 350

351 ISSKYQILFELCLGSFQ 367
|||||
351 ISSKYQILFELCLGSFQ 367
```

FIG. 40 (Cont.¹)

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230 LFTLLVETFFPERRYFYWYTIIGWGTPVCVTVWATLRLYFDDTGCDMN 279
|||||
251 LFTLLVETFFPERRYFYWYTIIGWGTPVCVTVWATLRLYFDDTGCDMN 300
|||||
280 DSTALWWVIKGPVVG SIMVNFVLFIGIIVILVQKLQSPDMGNESSIYLR 329
|||||
301 DSTALWWVIKGPVVG SIMVNFVLFIGIIVILVQKLQSPDMGNESSIYLR 350
|||||
330 LARSTLLIPLFGIHYTVFAFSPENVSKRERLVFELGLGSFQGFVVAVLY 379
|||||
351 LARSTLLIPLFGIHYTVFAFSPENVSKRERLVFELGLGSFQGFVVAVLY 400
|||||
380 CFLNGEVQAEIKRKWRSWKVNRYFAVDFKHRHPSLASSGVNNGGTQLSILS 429
|||||
401 CFLNGEVQAEIKRKWRSWKVNRYFAVDFKHRHPSLASSGVNNGGTQLSILS 450
|||||
430 KSSSQIRMSG LPADNLAT 447
|||||
451 KSSSQIRMSG LPADNLAT 468
|||||

FIG. 41 (CONT.¹)

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1 MERGLPLLCAVLALVAPAGAFRNDCEGDTIKIESPGYLTSYGPHSYHP 50
51 SEKCEWLIQAPDPYQRIMINFNPHFLEDRDCKYDYVEVFDGENENGHFR 100
|||||
51 SEKCEWLIQAPDPYQRIMINFNPHFLEDRDCKYDYVEVFDGENENGHFR 100
101 GKFCGKIAPPPVSSGPFLLFIKFVSDYETHGAGFSIRYEIFKRGPECSQN 150
|||||
101 GKFCGKIAPPPVSSGPFLLFIKFVSDYETHGAGFSIRYEIFKRGPECSQN 150
151 YTPSGVIKSPGFPEKYPNSLECTYIVFAPKMSEIILEFESFDLEPDSNP 200
|||||
151 YTPSGVIKSPGFPEKYPNSLECTYIVFAPKMSEIILEFESFDLEPDSNP 200
201 PGMFCRYDRLEIWDGFPDVGPHIGRYCGQKTPGRIRSSSGILSMVFYTD 250
|||||
201 PGMFCRYDRLEIWDGFPDVGPHIGRYCGQKTPGRIRSSSGILSMVFYTD 250

FIG. 43

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501 VYQRAVMAVGSLTINEERSEVDFSVPFVETGISVMVSRNGTVSPSAFL 550
|||||
501 VYQRAVMAVGSLTINEERSEVDFSVPFVETGISVMVSRNGTVSPSAFL 550
551 EPFSASVWMMFVMLLIVSAIAVFVFEEYFSPVGYNRNLA KGKAPHGPSFT 600
|||||
551 EPFSASVWMMFVMLLIVSAIAVFVFEEYFSPVGYNRNLA KGKAPHGPSFT 600
601 IGKAIWLLWGLVFNNSPVQNPKGTTSKIMVSVWAFFAVIFLASYTANLA 650
|||||
601 IGKAIWLLWGLVFNNSPVQNPKGTTSKIMVSVWAFFAVIFLASYTANLA 650
651 AFMIQEEFVDQVTGLSDKKFQRP HDYSPPFREGTVPNGSTERNIRNNYPY 700
|||||
651 AFMIQEEFVDQVTGLSDKKFQRP HDYSPPFREGTVPNGSTERNIRNNYPY 700

FIG. 44 (CONT. ²)

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701	MHQM	TKFNQK	VEDALV	SLKTGK	LDAFIY	DAAVLN	YKAGRDE	GCKLVTI	750
701	MHQM	TKFNQK	VEDALV	SLKTGK	LDAFIY	DAAVLN	YKAGRDE	GCKLVTI	750
751	GSYI	FATTGY	GIALQK	GPWKQ	IDLALLQ	FVGDM	EETLWLT	GIC	800
751	GSYI	FATTGY	GIALQK	GPWKQ	IDLALLQ	FVGDM	EETLWLT	GIC	800
801	HNEK	NEVMSS	QDIDNM	AGVFYML	AAAMALS	LITFI	WEHLFY	WKLRFCFT	850
801	HNEK	NEVMSS	QDIDNM	AGVFYML	AAAMALS	LITFI	WEHLFY	WKLRFCFT	850
851	GVCS	DRPGLL	FSISRG	IYSCIH	GVHIEE	KKKSPD	FNLTGS	QSNMLKLLRS	900
851	GVCS	DRPGLL	FSISRG	IYSCIH	GVHIEE	KKKSPD	FNLTGS	QSNMLKLLRS	900
901	AKNI	SSMSNM	NSSRMD	SPKRAAD	FIQ	RGSLIM	DVSDKGN	LMYSDNRSFQ	950
901	AKNI	SSMSNM	NSSRMD	SPKRAAD	FIQ	RGSLIM	DVSDKGN	LMYSDNRSFQ	950

FIG. 44 (CONT.)³⁾

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```
. . . . .
951 GKESIFGDNMNELQTFVANRQKDNLNNNYVFQGGQHP LTLNESNPNTVEVAV 1000
|||||
951 GKESIFGDNMNELQTFVANRQKDNLNNNYVFQGGQHP LTLNESNPNTVEVAV 1000

. . . . .
1001 STESKANSRPRQLWKKSVD SIRQDSLQNPV SQRDEATAENRTHSLKSPR 1050
|||||
1001 STESKANSRPRQLWKKSVD SIRQDSLQNPV SQRDEATAENRTHSLKSPR 1050

. . . . .
1051 YLPEEMAHS D ISETSNRATCHREPDNSKNHKT KD NFKRSVASKYPKDCSE 1100
|||||
1051 YLPEEMAHS D ISETSNRATCHREPDNSKNHKT KD NFKRSVASKYPKDCSE 1100

. . . . .
1101 VERTYLKTKSSSPRDKIYTIDGEEKEPGFHLDPPQFVENVTLPENVDFPDP 1150
|||||
1101 VERTYLKTKSSSPRDKIYTIDGEEKEPGFHLDPPQFVENVTLPENVDFPDP 1150

. . . . .
1151 YQDPSENF RKGDSTLPMNRNPLHNEEGLSNNDQYKLYSKHFTLKDKGSPH 1200
|||||
1151 YQDPSENF RKGDSTLPMNRNPLHNEEGLSNNDQYKLYSKHFTLKDKGSPH 1200
```

FIG. 44 (CONT.⁴)

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```

1201 SETSERYRQNSTHCRSCLSNMPTYSGHFTMRSPFKCDACLRMGNLYDIDE 1250
      |||||
1201 SETSERYRQNSTHCRSCLSNMPTYSGHFTMRSPFKCDACLRMGNLYDIDE 1250
      .
1251 DQMLQET..... 1257
      |||||
1251 DQMLQETGNPATGEQVYQQDWAQNNALQLQKNKLRI SRQHSYDNI VDKPR 1300
      .
      .
      .
1258 .....RDDQRLVIGRCPSDPYKHS LPSQAVNDSY 1286
      |||||
1351 SKRSKSLPDHTSDNPF LSHRDDQRLVIGRCPSDPYKHS LPSQAVNDSY 1400
      .
1287 LRSSLRSTASYCSRDSRGHNDVYISEHVMPYAANKNNMYSTPRVLNCSN 1336
      |||||
1401 LRSSLRSTASYCSRDSRGHNDVYISEHVMPYAANKNNMYSTPRVLNCSN 1450
      .
      1337 RRVYKKMPSIESDV 1350
      |||||
      1451 RRVYKKMPSIESDV 1464

```

FIG. 44 (CONT. ⁵)

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1 MRTLLPPALLTCWLLAPVNSIHPECRHFHLEIQEEETKCXELLRSQTEKHK 50
|||||
1 MRTLLPPALLTCWLLAPVNSIHPECRHFHLEIQEEETKCAELLRSQTEKHK 50

51 ACSGVWDNITCWRPANVGETVTVPCPKVFSNFYSKAGNISKNCTSDGWSE 100
|||||
51 ACSGVWDNITCWRPANVGETVTVPCPKVFSNFYSKAGNISKNCTSDGWSE 100

101 TFPDFVDACGYSDPEDESKITFYILVKAIYTLGYSVSLMSLATGSIILCL 150
|||||
101 TFPDFVDACGYSDPEDESKITFYILVKAIYTLGYSVSLMSLATGSIILCL 150

151 FRKLHCTRNYIHLNLFSLFILRAISVLVKDDVLYSSSGTLHCPDQPSWV 200
|||||
151 FRKLHCTRNYIHLNLFSLFILRAISVLVKDDVLYSSSGTLHCPDQPSWV 200

201 GCKLSLVFLQCYCIMANFFWLLVEGLYLHTLLVAMLPPrRCFLAYLLIGWG 250
|||||
201 GCKLSLVFLQCYCIMANFFWLLVEGLYLHTLLVAMLPPrRCFLAYLLIGWG 250

FIG. 45

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251 LPTVCIGAWTAARLYLEDTCWCWDTNDHSPVWVIRIPILISIIIVNFVLEI 300
|||||
251 LPTVCIGAWTAARLYLEDTCWCWDTNDHSPVWVIRIPILISIIIVNFVLEI 300
301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLLIPLFGVHYMVFAVFPIS 350
|||||
301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLLIPLFGVHYMVFAVFPIS 350
351 ISSKYQILFELCLGSGFQGLVVAVLYCFLNSEV 382
|||||
351 ISSKYQILFELCLGSGFQGLVVAVLYCFLNSEV 382

FIG. 45 (CONT.¹)

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1 MRTLLPPALLTCWLLAPVNSIHPECRFHLEIQEEETKCXELLRSQTEKHK 50
|||||
1 MRTLLPPALLTCWLLAPVNSIHPECRFHLEIQEEETKCAELLRSQTEKHK 50
|||||
51 ACSGVWDNITCWRPANVGETVTPCPKVFNFYSKAGNISKNCTSDGWSE 100
|||||
51 ACSGVWDNITCWRPANVGETVTPCPKVFNFYSKAGNISKNCTSDGWSE 100
|||||
101 TFPDFVDACGYSDPEDESKITFYILVKAIYTLGYSVSLMSLATGSIILCL 150
|||||
101 TFPDFVDACGYSDPEDESKITFYILVKAIYTLGYSVSLMSLATGSIILCL 150
|||||
151 FRKLHCTRNYIHLNLFSLFILLRAISVLVKDDVLYSSSGTLHCPDQPSSWV 200
|||||
151 FRKLHCTRNYIHLNLFSLFILLRAISVLVKDDVLYSSSGTLHCPDQPSSWV 200
|||||
201 GCKLSLVFLQYCIMANFFWLLVEGLYLHTLLVAMPLPRRCFLAYLLIGWG 250
|||||
201 GCKLSLVFLQYCIMANFFWLLVEGLYLHTLLVAMPLPRRCFLAYLLIGWG 250

FIG. 46

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251 LPTVCIGAWTAARLYLEDTCGWDNDHSDVPWWVIRIPILISIIVNEVLEFI 300
|||||
251 LPTVCIGAWTAARLYLEDTCGWDNDHSDVPWWVIRIPILISIIVNEVLEFI 300
301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLLIPLFGVHYMVFAVEFPIS 350
|||||
301 SIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLLIPLFGVHYMVFAVEFPIS 350
351 ISSKYQILFELCLGSGFQGLVVAVLYCFLNSEV 382
|||||
351 ISSKYQILFELCLGSGFQGLVVAVLYCFLNSEV 382

FIG. 46 (CONT.¹)

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```

1  MKSGSGGSPTSLWGLLFLSAALSLWPTSGEICGPGIDIRNDYQQLKRLE  50
   |||||||
1  MKSGSGGSPTSLWGLLFLSAALSLWPTSGEICGPGIDIRNDYQQLKRLE  50

51 NCTVIEGYLHILLISKAEDYRSYRFPKLTVITEYLLFRVAGLESGLDLF  100
   |||||||
51 NCTVIEGYLHILLISKAEDYRSYRFPKLTVITEYLLFRVAGLESGLDLF  100

101 PNLTVIRGWKLFYNYALVIFEMTNLKDIGLYNLRNITRGAIRIEKNADLC  150
   |||||||
101 PNLTVIRGWKLFYNYALVIFEMTNLKDIGLYNLRNITRGAIRIEKNADLC  150

151 YLSTVDWSLILDVSNNNYIVGNKPPKECGDLCPGTMEЕКPMCEKTTINNE  200
   |||||||
151 YLSTVDWSLILDVSNNNYIVGNKPPKECGDLCPGTMEЕКPMCEKTTINNE  200

201 YNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGSCSAPDNDTACVA  250
   |||||||
201 YNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGSCSAPDNDTACVA  250

```

FIG. 47

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501 SKNRIITWHRYRPPDYRDLISFTVYYKEAPFKNVTEYDGDACGSNSWN 550
|||||
501 SKNRIITWHRYRPPDYRDLISFTVYYKEAPFKNVTEYDGDACGSNSWN 550
551 MVDVDLPPNKDVEPGILLHGLKPWTQYAVYVKAATLTMVENDHIRGAKSE 600
|||||
551 MVDVDLPPNKDVEPGILLHGLKPWTQYAVYVKAATLTMVENDHIRGAKSE 600
601 ILYIRTNASVPSIPLDVLSASNSSQLIVKWNPPSLPNGNLSYYIVRWQR 650
|||||
601 ILYIRTNASVPSIPLDVLSASNSSQLIVKWNPPSLPNGNLSYYIVRWQR 650
651 QPQDGYLYRHNYCSKDKIPIRKYADGTIDIEEVTENPKTEVCGGEGPCC 700
|||||
651 QPQDGYLYRHNYCSKDKIPIRKYADGTIDIEEVTENPKTEVCGGEGPCC 700
701 ACPKTEAEKQAEKEEAEYRKVFENFLHNSIFVPRPERKRRDVMQVANTTM 750
|||||
701 ACPKTEAEKQAEKEEAEYRKVFENFLHNSIFVPRPERKRRDVMQVANTTM 750

FIG. 47 (CONT.²)

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1001 MSRELQGSFGMVYEGVAKGVKDEPETRVAIKTVNEAASMRRERIEFLNE 1050
|||||
1001 MSRELQGSFGMVYEGVAKGVKDEPETRVAIKTVNEAASMRRERIEFLNE 1050

1051 ASVMKEFNCHHVRLLGVSQGGQPTLVIMELMTRGDLKSYLSLRPEMEN 1100
|||||
1051 ASVMKEFNCHHVRLLGVSQGGQPTLVIMELMTRGDLKSYLSLRPEMEN 1100

1101 NPVLAPPSLSKMIQAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVK 1150
|||||
1101 NPVLAPPSLSKMIQAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVK 1150

1151 IGDFGMTRDIYETDYRKGGKGLLPVRWMSPESLKDGVTYSDVWSFGV 1200
|||||
1151 IGDFGMTRDIYETDYRKGGKGLLPVRWMSPESLKDGVTYSDVWSFGV 1200

1201 VLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPDNCPDMLFELMRMCWQ 1250
|||||
1201 VLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPDNCPDMLFELMRMCWQ 1250

FIG. 47 (CONT.⁴)

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1251 YNPKMRPSFLEIISSIK.....EELDLEPENM 1277
|||||
1251 YNPKMRPSFLEIISSIKEEMEPGFREVSVFYSEENKLPEPEELDLEPENM 1300
1278 ESVPLDPSASSSSSLPLPDRHSGHKAENGPGVGLVLRASFDERQPYAHMN 1327
|||||
1301 ESVPLDPSASSSSSLPLPDRHSGHKAENGPGVGLVLRASFDERQPYAHMN 1350
1328 GGRKNERALPLPQSSSTC 1344
|||||
1351 GGRKNERALPLPQSSSTC 1367

FIG. 47 (CONT.⁵)

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1 MERGLPLLCAVLALVAPAGAFRNDKCGDTIKIESPGYLTSYGPHSYHP 50
|||||
1 MERGLPLLCAVLALVAPAGAFRNDKCGDTIKIESPGYLTSYGPHSYHP 50
51 SEKCEWLIQAPDPYQRIMINFNPHFDLEDNRDCKYDYVEVFDGENENEGHFR 100
|||||
51 SEKCEWLIQAPDPYQRIMINFNPHFDLEDNRDCKYDYVEVFDGENENEGHFR 100
101 GKFCGKIAPPPVSSGPFLEIKFVSDYETHGAGFSIRYEI FKRGPESCSQ 150
|||||
101 GKFCGKIAPPPVSSGPFLEIKFVSDYETHGAGFSIRYEI FKRGPESCSQ 150
151 YTPSGVIKSPGFPEKYPNSLECTYIVFAPKMSEIILEFESFDLEPDSNP 200
|||||
151 YTPSGVIKSPGFPEKYPNSLECTYIVFAPKMSEIILEFESFDLEPDSNP 200
201 PGGMFCRYDRLEIWDGFPDVGPHIGRYCGQKTPGRIRSSSGILSMVFYTD 250
|||||
201 PGGMFCRYDRLEIWDGFPDVGPHIGRYCGQKTPGRIRSSSGILSMVFYTD 250

FIG. 48

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251 SAIKEGFSANYSVLQSSVSEDFKCMEALMESGEIHSDQITASSQYSTN 300
|||||
251 SAIKEGFSANYSVLQSSVSEDFKCMEALMESGEIHSDQITASSQYSTN 300
301 WSAERSRLNYPENGWTPGEDSYREWIQVDLGLLRFVTAVGTOGAISKETK 350
|||||
301 WSAERSRLNYPENGWTPGEDSYREWIQVDLGLLRFVTAVGTOGAISKETK 350
351 KKYVVKTYKIDVSSNGEDWITKEGNKPVLFQGNTPD VVAVFPKPLI 400
|||||
351 KKYVVKTYKIDVSSNGEDWITKEGNKPVLFQGNTPD VVAVFPKPLI 400
401 TRFVRIKPATWETGISMRFEVYGCKITDYPCSGMLGMVSLISDSQITSS 450
|||||
401 TRFVRIKPATWETGISMRFEVYGCKITDYPCSGMLGMVSLISDSQITSS 450
451 NQGDRNWMPENIRLVTSRSGWALPPAPHSYINELQIDLGEKIVRGIII 500
|||||
451 NQGDRNWMPENIRLVTSRSGWALPPAPHSYINELQIDLGEKIVRGIII 500

FIG. 48 (CONT.¹)

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501 QGGKHRENKVFMRKFKIGYSNNGSDWKIMIMDDSKRKAKSFEGNNNYDTPE 550
|||||
501 QGGKHRENKVFMRKFKIGYSNNGSDWKIMIMDDSKRKAKSFEGNNNYDTPE 550
551 LRTPALSTRFIRIYPERATHGGLGLRMELLGCEVEAPTAGPTTPNGNLV 600
|||||
551 LRTPALSTRFIRIYPERATHGGLGLRMELLGCEVEAPTAGPTTPNGNLV 600
601 DECDDDDQANCHSGTGDDFQLTG GTTVLATEKPTVIDSTIQS 641
|||||
601 DECDDDDQANCHSGTGDDFQLTG GTTVLATEKPTVIDSTIQS 641

FIG. 48 (CONT.²)

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1 MERGLPLLCAVLALVAPAGAFRNDKCGDTIKIESPGYLTSPPGYPHSYHP 50
|||||
1 MERGLPLLCAVLALVAPAGAFRNDKCGDTIKIESPGYLTSPPGYPHSYHP 50

51 SEKCEWLIQAPDPYQIRIMINFNPHFDLEDRCCKYDYVEVFDGENENGHFR 100
|||||
51 SEKCEWLIQAPDPYQIRIMINFNPHFDLEDRCCKYDYVEVFDGENENGHFR 100

101 GKFCGKIAPPPVVSSGPFLLFIKFVSDYETHGAGFSIRYEIFKRGPECSQN 150
|||||
101 GKFCGKIAPPPVVSSGPFLLFIKFVSDYETHGAGFSIRYEIFKRGPECSQN 150

151 YTPSGVIKSPGFPEKYPNSLECTYIVFAPKMSEIILEFESFDLEPDSNP 200
|||||
151 YTPSGVIKSPGFPEKYPNSLECTYIVFAPKMSEIILEFESFDLEPDSNP 200

201 PGGMFCRYDRLEIWDGFPDVGPHIGRYCGQKTPGRIRSSSGILSMVFYTD 250
|||||
201 PGGMFCRYDRLEIWDGFPDVGPHIGRYCGQKTPGRIRSSSGILSMVFYTD 250

FIG. 49

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501 OGGKHRENKVFMRKEKIGYSNNGSDWKMIIMDDSKRKAK..... 538

[illegible]

501 OGGKHRENKVFMRKEKIGYSNNGSDWKMIIMDDSKRKAKEGNNNYDTP 550

1

539
GGTTVLATEKPTVIDSTIQSEFFPTYGNC 567

601 DECDDQANCHSGTGDDFQLTGGTTLATEKPTVIDSTIQSEFFPTYGNC 650

568 EFGWGS HKTFCHWEHDNHVQLKWSVLTSTKGTPIQDHTGDNFIYSQADEN 617

651 EFGWGSHTTFCHWEHDNHVQLKWSVLTSTKTGPIQDHTGDNFIYSQADEN 700

618 OKGKVARLVSPVVYSONSAHCMTFWYHMSGSHVGTLRVKLRYYQKPPEEYDQ 667

[illegible]

701 OKGKVARLVSPVVYSONSAHCMTFWYHMSGSHVGTLRVKLRYPQPEEYDQ 750

FIG. 49 (CONT.²)

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```

668 LVWMAIGHQGDHWKEGRVLLHKSLKLYQVIFEEGEIGKGNLGGIAVDDISI 717
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
751 LVWMAIGHQGDHWKEGRVLLHKSLKLYQVIFEEGEIGKGNLGGIAVDDISI 800
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
718 NNHISQEDCAKPADLDKKNPEIKIDETGSTPGYEGEGEDKNISRKPGENV 767
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
801 NNHISQEDCAKPADLDKKNPEIKIDETGSTPGYEGEGEDKNISRKPGENV 850
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
768 LKTLXPILITIIAMSA LGVLLGAVCGVVLYCACWHNGMSE RNLSALENYN 817
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
851 LKTLXPILITIIAMSA LGVLLGAVCGVVLYCACWHNGMSE RNLSALENYN 900
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
818 FELVDGVKLLKKDKLNTQSTYSEA 840
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
901 FELVDGVKLLKKDKLNTQSTYSEA 923

```

FIG. 49 (CONT.³)

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```

1 MERGLPLLCVALLVAPAGAFRNDKCGDTIKIESPGYLTPGYPHSYHP 50
|||||
1 MERGLPLLCVALLVAPAGAFRNDKCGDTIKIESPGYLTPGYPHSYHP 50
.
51 SEKCEWLIQAPDPYQIRIMINFNPHFDLEDRDCKYDYVEVFDGENENGHFR 100
|||||
51 SEKCEWLIQAPDPYQIRIMINFNPHFDLEDRDCKYDYVEVFDGENENGHFR 100
.
101 GKFCGKIAPPPVSSGPFLLFIKVFSDYETHGAGFSIRYEIIFKRGPECSQN 150
|||||
101 GKFCGKIAPPPVSSGPFLLFIKVFSDYETHGAGFSIRYEIIFKRGPECSQN 150
.
151 YTPSGVIKSPGFPEKYPNSLECTYIVFAPKMSIILEFESFDLEPDSNP 200
|||||
151 YTPSGVIKSPGFPEKYPNSLECTYIVFAPKMSIILEFESFDLEPDSNP 200
.
201 PGGMFCRYDRLEIWDGFPDVGPHIGRYCGQKTPGRIRSSSGILSMVFYTD 250
|||||
201 PGGMFCRYDRLEIWDGFPDVGPHIGRYCGQKTPGRIRSSSGILSMVFYTD 250
.
251 SAIAKEGFSANYSVLQSSVSEDFKCMEALGMESGEIHSDQITASSQYSTN 300
|||||
251 SAIAKEGFSANYSVLQSSVSEDFKCMEALGMESGEIHSDQITASSQYSTN 300

```

FIG. 50

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301	WSAERSRLNYPENGWTPGEDSYREWIQVDLGLLRFVTA	350
	VGTSKQGAISKETK	
301	WSAERSRLNYPENGWTPGEDSYREWIQVDLGLLRFVTA	350
	VGTSKQGAISKETK	
351	KKYYVKTYKIDVSSNGEDWITIKEGNKPVL	400
	FQGNTPD	
351	KKYYVKTYKIDVSSNGEDWITIKEGNKPVL	400
	FQGNTPD	
401	TRFVRIKPATWETGISMRFEVYGCKITDYPCSGMLGMV	450
	SGLISDSQITSS	
401	TRFVRIKPATWETGISMRFEVYGCKITDYPCSGMLGMV	450
	SGLISDSQITSS	
451	NQGDRNWMPENIRLVTSRSGWALPPAPHSYIN	500
	EWLQIDLGECKIVRGII	
451	NQGDRNWMPENIRLVTSRSGWALPPAPHSYIN	500
	EWLQIDLGECKIVRGII	
501	QGGKHRENKVFMRKFKIGYSNNGSDWKIMDDSKRKAR	538
501	QGGKHRENKVFMRKFKIGYSNNGSDWKIMDDSKRKAK	538

FIG. 50 (CONT.¹)

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1 MGAPACALALCVAVAIVAGASSESLGTEQVRVVGRAAEVPGPEQGQEQLV 50
|||||
1 MGAPACALALCVAVAIVAGASSESLGTEQVRVVGRAAEVPGPEQGQEQLV 50

51 FGSGDAVELSCPPPGGGPMGPTVWVKDGTGLVPSEVLVGPQRLQVLNAS 100
|||||
51 FGSGDAVELSCPPPGGGPMGPTVWVKDGTGLVPSEVLVGPQRLQVLNAS 100

101 HEDSGAYSCRQRLTQRVLCHFVSRVTDAPSSGDDEDEGEAEEDTGVDTGA 150
|||||
101 HEDSGAYSCRQRLTQRVLCHFVSRVTDAPSSGDDEDEGEAEEDTGVDTGA 150

151 PYWTRPERMDKLLAVPAANTVFRCPAAGNPTPSISWLKNGREFRGEHR 200
|||||
151 PYWTRPERMDKLLAVPAANTVFRCPAAGNPTPSISWLKNGREFRGEHR 200

201 IGGIKLRHQQWSLVMESVVPSPDRGNVTCVVENKFGSIRQTYTLDVLERSP 250
|||||
201 IGGIKLRHQQWSLVMESVVPSPDRGNVTCVVENKFGSIRQTYTLDVLERSP 250

FIG. 51

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251 DLIQCYNFGWYPESPICEGRRNRCPPPPVPLNSKIQPHSTTYRHGERVHI 300
|||||
251 DLIQCYNFGWYPESPICEGRRNRCPPPPVPLNSKIQPHSTTYRHGERVHI 300
301 ECELNFVIQSGSEELLCENGKWTETPKCI 328
|||||
301 ECELNFVIQSGSEELLCENGKWTETPKCI 328

FIG. 52 (CONT.¹)

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1 MPWGRRPTWLLAFLLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50
|||||
1 MPWGRRPTWLLAFLLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50
51 PAPFLVFSQGKSI SRIDPDGTNHQQLVVDAGISADMDIHYKKERLYWVDV 100
|||||
51 PAPFLVFSQGKSI SRIDPDGTNHQQLVVDAGISADMDIHYKKERLYWVDV 100
101 ERQVLLRVFLNGTGLEKVCNVERKVSGLAIDWIDDEVLWVDQQNGVITVT 150
|||||
101 ERQVLLRVFLNGTGLEKVCNVERKVSGLAIDWIDDEVLWVDQQNGVITVT 150
151 DMTGKNSRVLLSSLKHPSNIAVDPIERLMFWSSEVTGSLHRAHLKGVDVK 200
|||||
151 DMTGKNSRVLLSSLKHPSNIAVDPIERLMFWSSEVTGSLHRAHLKGVDVK 200
201 TLLETGGISVLTLDVLDKRLFWVQDSGEGSHAYIHSCDYEGGSVRLIRHQ 250
|||||
201 TLLETGGISVLTLDVLDKRLFWVQDSGEGSHAYIHSCDYEGGSVRLIRHQ 250
251 ARHSLSSMAFFGDRIFYSVLKSKAIWIANKHTGKDTVRINLHPSFVTPGK 300
|||||
251 ARHSLSSMAFFGDRIFYSVLKSKAIWIANKHTGKDTVRINLHPSFVTPGK 300

FIG. 53

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301 LMVVHPRAQPRTEAAKDPDPPELLKQGRGPCRFGLCERDPKSHSSACAEG 350
|||||
301 LMVVHPRAQPRTEAAKDPDPPELLKQGRGPCRFGLCERDPKSHSSACAEG 350
|||||
351 YTLSDRKYCEDVNECATQNHGCTLGCENTPGSYHCTCPTGFVLLPDGKQ 400
|||||
351 YTLSDRKYCEDVNECATQNHGCTLGCENTPGSYHCTCPTGFVLLPDGKQ 400
|||||
401 CHELVSCPGNVSKCSHGCVLTSDGPRCICFAGSVLGRDGKTCTGCSSPDN 450
|||||
401 CHELVSCPGNVSKCSHGCVLTSDGPRCICFAGSVLGRDGKTCTGCSSPDN 450
|||||
451 GGCSQICLPLRPGSWECDCFPGYDLQSDRKSCAASGPQPLLFFANSQDIR 500
|||||
451 GGCSQICLPLRPGSWECDCFPGYDLQSDRKSCAASGPQPLLFFANSQDIR 500
|||||
501 HMFEDGTDYKVLLSRQMGVMVFALDYPDVESKIYFAQTALKWIERANMDGS 550
|||||
501 HMFEDGTDYKVLLSRQMGVMVFALDYPDVESKIYFAQTALKWIERANMDGS 550
|||||
551 QRERLITEGVDTLEGLALDWIGRRIYWTDSGKSVVGGSDLGKHHRIIQ 600
|||||
551 QRERLITEGVDTLEGLALDWIGRRIYWTDSGKSVVGGSDLGKHHRIIQ 600

FIG. 53 (CONT. ¹)

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601	ERISRPRGIAVHPRARRLFWTDVGMSPRIESASLQGS	DRVLIASSNLL	650
601	ERISRPRGIAVHPRARRLFWTDVGMSPRIESASLQGS	DRVLIASSNLL	650
651	SGITIDYLTDTLYWC	DKRSVIEMANLDGSKRRRLIQNDVGHPFSLAVFE	700
651	SGITIDYLTDTLYWC	DKRSVIEMANLDGSKRRRLIQNDVGHPFSLAVFE	700
701	DHLWVSDWAIPSVIRVNKRTGQNRVRLQGSM	LKPSSLVVHPLAKPGADP	750
701	DHLWVSDWAIPSVIRVNKRTGQNRVRLQGSM	LKPSSLVVHPLAKPGADP	750
751	CLYRNGGCEHICQESLGTARCLCREGFVKAWDG	KMCLPDYPILSGENAD	800
751	CLYRNGGCEHICQESLGTARCLCREGFVKAWDG	KMCLPDYPILSGENAD	800
801	LSKEVTSLSNSTQAEVPDDDGTESTLVAE	IMVSGMNYEDDCGPGCGSH	850
801	LSKEVTSLSNSTQAEVPDDDGTESTLVAE	IMVSGMNYEDDCGPGCGSH	850
851	ARCVSDGETAECQCLKGFARDGNLCS	DIDECVLARSDCPSTSSRCINTEG	900
851	ARCVSDGETAECQCLKGFARDGNLCS	DIDECVLARSDCPSTSSRCINTEG	900

FIG. 53 (CONT. 2)

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```

851  ARCVSDGETAECQCLKG FARDGNLCSDIDECVLARSDCPSTSSRCINTEG 900
      |||||
851  ARCVSDGETAECQCLKG FARDGNLCSDIDECVLARSDCPSTSSRCINTEG 900

      .
901  GYVCRCEGYEGDGI SCFDIDECQRGAHNCAENAACTNTEGGYNCTCAGR 950
      |||||
901  GYVCRCEGYEGDGI SCFDIDECQRGAHNCAENAACTNTEGGYNCTCAGR 950

      .
951  PSSPGLSCP DSTAPSL LGEDGHHLDRNSYPGCPSSYDGYCLNGVCMHIE 1000
      |||||
951  PSSPGRSCP DSTAPSL LGEDGHHLDRNSYPGCPSSYDGYCLNGVCMHIE 1000

      .
1001 SLD SYTCNCVIGYSGDRCQT..... 1020
      |||||

1001 SLD SYTCNCVIGYSGDRCQTRDLRWELRHAGYGQKH DIMVVAVCMVALV 1050

      .
1021 .....PPSSDRGPQEIEGNSHLPSYRPPVGPEKLHSLQSANG 1056
      |||||

1151 PHIDGMGTGQSCWIPPSDDRGPEIEGNSHLPSYRPPVGPEKLHSLQSANG 1200

      .
      1057 SCHERAPDLPRQTEPVQ 1073
          |||||
      1201 SCHERAPDLPRQTEPVK 1217

```

Fig. 53 (Cont.³)

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1 MPWRRPTWLLAFLLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50
|||||
1 MPWRRPTWLLAFLLVFLKISILSVTAWQTGNCQPGPLERSERSGTCAG 50
51 PAPFLVFSQGKSI SRIDPDGTNHQQLVVDAGISADMDIHYKKERLYWVDV 100
|||||
51 PAPFLVFSQGKSI SRIDPDGTNHQQLVVDAGISADMDIHYKKERLYWVDV 100
101 ERQVLLRVFLNGTGLEKVCNVERKVSGLAIDWIDDEVLWVDQQNGVITVT 150
|||||
101 ERQVLLRVFLNGTGLEKVCNVERKVSGLAIDWIDDEVLWVDQQNGVITVT 150
151 DMTGKNSRVLLSSLKHPSNIAVDPIERLMFWSSEVTGSLHRAHLKGVDVK 200
|||||
151 DMTGKNSRVLLSSLKHPSNIAVDPIERLMFWSSEVTGSLHRAHLKGVDVK 200
201 TLLETGGISVLTLDVLDKRLFWVQDSGEGSHAYIHSCDYEGGSVRLIRHQ 250
|||||
201 TLLETGGISVLTLDVLDKRLFWVQDSGEGSHAYIHSCDYEGGSVRLIRHQ 250

FIG. 54

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251 ARHSLSSMAFFGDRIFYSVLKSKAIWIA NKHTGKDTVRLNHP SFVTPGK 300
|||||
251 ARHSLSSMAFFGDRIFYSVLKSKAIWIA NKHTGKDTVRLNHP SFVTPGK 300
|||||
301 LMVVHPRAQPRTEDAAKDPDP ELLKQGRGPCRFGLCERDPKSHSSACAEG 350
|||||
301 LMVVHPRAQPRTEDAAKDPDP ELLKQGRGPCRFGLCERDPKSHSSACAEG 350
|||||
351 YTLSRDRKYCEDVNECATQNHGCTLGCENTPGSYHCTCPTGFVLLPDGKQ 400
|||||
351 YTLSRDRKYCEDVNECATQNHGCTLGCENTPGSYHCTCPTGFVLLPDGKQ 400
|||||
401 CHELVSCPGNVSKCSHGCVLTSDGPRCICFAGSVLGRDGTCTGCSSPDN 450
|||||
401 CHELVSCPGNVSKCSHGCVLTSDGPRCICFAGSVLGRDGTCTGCSSPDN 450
|||||
451 GGCSQICLPLRPGSWECD CFPGYDLQSDRKSCAASGPQPLL FANSQDIR 500
|||||
451 GGCSQICLPLRPGSWECD CFPGYDLQSDRKSCAASGPQPLL FANSQDIR 500
|||||

FIG. 54 (CONT. ¹)

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501 HMHFDGTDYKVLLSRQMGVMFALDYPDVESKIYFAQTALKWIERANMDGS 550
|||||
501 HMHFDGTDYKVLLSRQMGVMFALDYPDVESKIYFAQTALKWIERANMDGS 550
|||||
551 QRERLITEGVDTLEGLALDWIGRRRIYWTDSGKSVVGSDLSGKHHRIIQ 600
|||||
551 QRERLITEGVDTLEGLALDWIGRRRIYWTDSGKSVVGSDLSGKHHRIIQ 600
|||||
601 ERISRPRGIAVHPRARRLFWTDVGMSPRIESASLQGSDDRVLIASSNLLEP 650
|||||
601 ERISRPRGIAVHPRARRLFWTDVGMSPRIESASLQGSDDRVLIASSNLLEP 650
|||||
651 SGITIDYLTDTLYWCDDTKRSVIEMANLDGSKRRRLIQNDVGHPFSLAVFE 700
|||||
651 SGITIDYLTDTLYWCDDTKRSVIEMANLDGSKRRRLIQNDVGHPFSLAVFE 700
|||||
701 DHLWVSDWAIPSVIRVNKRTGQNRVRLQGSMLKPPSSLVVVHPLAKPGADP 750
|||||
701 DHLWVSDWAIPSVIRVNKRTGQNRVRLQGSMLKPPSSLVVVHPLAKPGADP 750
|||||
751 CLYRNGGCEHICQESLGTARCLCREGEVKAWDGKMCLPQDYPILSGENA 799
|||||
751 CLYRNGGCEHICQESLGTARCLCREGEVKAWDGKMCLPQDYPILSGENA 799
|||||

FIG. 54 (CONT. ²)

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210 ARCVSDGETAECQCLKGFARDGNLCSIDIECVLARSDCPSTSSRCINTEG 259
|||||
851 ARCVSDGETAECQCLKGFARDGNLCSIDIECVLARSDCPSTSSRCINTEG 900
260 GYVCRCEGYEGDGISCFDIECQRGAHNCAENAACTNTEGGYNCTCAGR 309
|||||
901 GYVCRCEGYEGDGISCFDIECQRGAHNCAENAACTNTEGGYNCTCAGR 950
310 PSSPGLSCPDPSTAPSLLGEDGHHLDRNSYPGCPSSYDGYCLNGGVCMHIE 359
|||||
951 PSSPGRSCPDPSTAPSLLGEDGHHLDRNSYPGCPSSYDGYCLNGGVCMHIE 1000
360 SLDSYTCNCVIGYSGDRCQTRDLRWWEHLRHAGYGQKHDIMVVAVCMVALV 409
|||||
1001 SLDSYTCNCVIGYSGDRCQTRDLRWWEHLRHAGYGQKHDIMVVAVCMVALV 1050
410 LLLLLGMWGTYYYRTRKQLSNPPKNPCDEPSGVSSSGPDSSSGAAVASC 459
|||||
1051 LLLLLGMWGTYYYRTRKQLSNPPKNPCDEPSGVSSSGPDSSSGAAVASC 1100

FIG. 55 (CONT. ¹)

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460 PQWFEVLEKHQDPKNGSLPADGTNGAVVDAGLSPLQLGSHLTSWRQK 509
 11101 PQWFEVLEKHQDPKNGSLPADGTNGAVVDAGLSPLQLGSHLTSWRQK 1150

510 PHIDGMGTGQSCWIPSSDRGPQIEGNSHLPSYRPVGPEKLHSLQSANG 559
 11151 PHIDGMGTGQSCWIPSSDRGPQIEGNSHLPSYRPVGPEKLHSLQSANG 1200

560 SCHERAPDLPRQTEPVQ 576
 1201 SCHERAPDLPRQTEPVK 1217

FIG. 55 (CONT. 2)

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251	QLEPLYNLHAYVRRALHRRYGDKYVNLRGPIPAHLLGDMWAQSWENIYD	300
251	QLEPLYNLHAYVRRALHRRYGDKYVNLRGPIPAHLLGDMWAQSWENIYD	300
301	MVVPFPDKPNLDVTSTMVQKGWNATHMFRVSEEFFTSGLSPMPPEFWAE	350
301	MVVPFPDKPNLDVTSTMVQKGWNATHMFRVSEEFFTSGLSPMPPEFWAE	350
351	SMLEKPTDGREVVCHASAWDFYNRKDFRIKQCTRVTMEQLATVHHEMGHV	400
351	SMLEKPTDGREVVCHASAWDFYNRKDFRIKQCTRVTMEQLATVHHEMGHV	400
401	QYYLQYKDLHVSLLRRGANPGFHEAIGDVLALS SVSTPAHLHKIGLLDHVTN	450
401	QYYLQYKDLHVSLLRRGANPGFHEAIGDVLALS SVSTPAHLHKIGLLDHVTN	450
451	DIESDINYLKMALEKIAFLPFGYLV DQWRWGVFSGRTPPSRYNFDWWYL	500
451	DIESDINYLKMALEKIAFLPFGYLV DQWRWGVFSGRTPPSRYNFDWWYL	500

FIG. 57 (CONT.)¹

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751 DMTTYSLSNICYTNGTCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVG 800
|||||
751 DMTTYSLSNICYTNGTCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVG 800
|||||
801 RAILPFFPKYVEFSNKKIANKLNGYTDAGDSWRSLYESDNLEQDLEKLYQEL 850
|||||
801 RAILPFFPKYVEFSNKKIANKLNGYTDAGDSWRSLYESDNLEQDLEKLYQEL 850
|||||
851 QPLYNLHAYVRRSLHRHYGSEYNLDGPIPAHLLGNMWAQTSNIYDLV 900
|||||
851 QPLYNLHAYVRRSLHRHYGSEYNLDGPIPAHLLGNMWAQTSNIYDLV 900
|||||
901 APFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSGLLPVPPEFWNKSM 950
|||||
901 APFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSGLLPVPPEFWNKSM 950
|||||
951 LEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMGIQY 1000
|||||
951 LEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMGIQY 1000
|||||

FIG. 57 (CONT.³)

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```

1001 FMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTEGSY 1050
|||||
1001 FMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTEGSY 1050

1051 EYDINFLMKMALDKIAFIPFSYLIDQWRWRVFDGSIITKENYNQEWWSLRL 1100
|||||
1051 EYDINFLMKMALDKIAFIPFSYLIDQWRWRVFDGSIITKENYNQEWWSLRL 1100

1101 KYQGLCPPVPRSQGFDPGSKFHVHPANVPYVRYFVSFIIQFQFHEALCRA 1150
|||||
1101 KYQGLCPPVPRSQGFDPGSKFHVHPANVPYVRYFVSFIIQFQFHEALCRA 1150

1151 AGHTGPLHKCDIYQSKEAGKLLADAMKLGYSKPWPEAMKLITGQPNMSAS 1200
|||||
1151 AGHTGPLHKCDIYQSKEAGKLLADAMKLGYSKPWPEAMKLITGQPNMSAS 1200

1201 AMMNYFKPLTEWLVTENRRRHGETLGWPEYNWAPNT 1235
|||||
1201 AMMNYFKPLTEWLVTENRRRHGETLGWPEYNWAPNT 1235

```

FIG. 57 (CONT. ⁴)

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1 MTMTLHTKASGMALLHQIQGNELEPLNRPQLKMPMERALGEVYVDNSKPT 50
|||||
1 MTMTLHTKASGMALLHQIQGNELEPLNRPQLKMPMERALGEVYVDNSKPT 50

51 VFNYPEGAAYEFNAAAAAASAPVYGQSGIAYGPGSEAAAFSANSLSGA 100
|||||
51 VFNYPEGAAYEFNAAAAAASAPVYGQSGIAYGPGSEAAAFSANSLSGA 100

101 FPQLNSVSPSPLMLLHPPPPQLSPFLHPHGQQVPYYLENEPSAYAVRDTGP 150
|||||
101 FPQLNSVSPSPLMLLHPPPPQLSPFLHPHGQQVPYYLENEPSAYAVRDTGP 150

151 PAFYRSNSDNRRQNGRERLSSSNEKGNMIMESAKETRYCAVCNDYASGYH 200
|||||
151 PAFYRSNSDNRRQNGRERLSSSNEKGNMIMESAKETRYCAVCNDYASGYH 200

FIG. 58

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200 PLCLPEKSFSENTLARIRFSRVSGWQLLDRGATALELMSIEVPRIMTQD 249
 |||||
 301 PLCLPEKSFSENTLARIRFSRVSGWQLLDRGATALELMSIEVPRIMTQD 350
 |||||
 250 CLEHAKHSSNTPKITENMFCAGYMDGTDCKDACKGDSGGPHATHYHGTWYLT 299
 |||||
 351 CLEHAKHSSNTPKITENMFCAGYMDGTDCKDACKGDSGGPHATHYHGTWYLT 400
 |||||
 300 GVVSWGEGCAAIGHIGVYTRVSQYIDWLVRHMDSKLQGVFRLPLL 345
 |||||
 401 GVVSWGEGCAAIGHIGVYTRVSQYIDWLVRHMDSKLQGVFRLPLL 446

FIG. 59 (CONT.)¹

```

1 MGFLKFSPFLVVSILL..... 17
| | | | | | | | | |
1 MGFLKFSPFLVVSILLYQACSLQAVPLRSILESSPGMATLSEEEVRLLA 50

18 ALVQDYMQMKA RELEEEEEQEAE GSSLDSPRSKRCGNLSTCMLGTYTQDL 67
| | | | | | | | | | | | | | | | | | | | | | | | | |
51 ALVQDYMQMKA RELEEEEEQEAE GSSLDSPRSKRCGNLSTCMLGTYTQDL 100

      .           .           .
68 NKFHTFPQT SIGVEAPGKKRDVAKDLETNHQSHFGN 103
   | | | | | | | | | | | | | | | | | | | |
101 NKFHTFPQT SIGVEAPGKKRDVAKDLETNHQSHFGN 136

```

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FIG. 60

```

1 MGFLKFSPFLVVSILL..... 17
| | | | | | | | | |
1 MGFLKFSPFLVVSILLYQACSLQAVPLRSILESSPGMATLSEEEVRLLA 50

18 ALVQDYMQMKA RELEEEEEQEAE GSSLDSPRSKRCGNLSTCMLGTYTQDL 67
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 ALVQDYMQMKA RELEEEEEQEAE GSSLDSPRSKRCGNLSTCMLGTYTQDL 100

      .           .           .
68 NKFHTFPQT SIGVEAPGKKRDVAKDLETNHQSHFGN 103
   | | | | | | | | | | | | | | | | | | | | | |
101 NKFHTFPQT SIGVEAPGKKRDVAKDLETNHQSHFGN 136

```


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301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMMNWTTHIAACVL 350
|||||
301 IDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMMNWTTHIAACVL 350
|||||
351 KGLFALVAYLTWADETKEVI.TDNLPGSIRAVVNFLVAKALLSYPLPFFA 400
|||||
351 KGLFALVAYLTWADETKEVI.TDNLPGSIRAVVNFLVAKALLSYPLPFFA 400
|||||
401 AVEVLEKSLFQEGSRAFFPACYGGDGRLLKSWELTLRCALVVFTLLMAIYV 450
|||||
401 AVEVLEKSLFQEGSRAFFPACYGGDGRLLKSWELTLRCALVVFTLLMAIYV 450
|||||
451 PHFALLMGLTGSLTGAGLCFLLPSLFHLRLWRKLLWHQVFFDVAFVIG 500
|||||
451 PHFALLMGLTGSLTGAGLCFLLPSLFHLRLWRKLLWHQVFFDVAFVIG 500
|||||
501 GICSVSGFVHSLEGLIEAYRT 521
|||||
501 GICSVSGFVHSLEGKFAGLET 521
|||||

FIG. 61 (CONT.¹)

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251 EKFVEWTRLDMMDEEEVEVSLPRFKLEESYDMESVLRNLGMTDAFELGKA 300
|||||
251 EKFVEWTRLDMMDEEEVEVSLPRFKLEESYDMESVLRNLGMTDAFELGKA 300
301 DFIGMSQTDLSLSKVVKHSFVEVNEEGTEAAAAATAAIMMRCARFVPRFC 350
|||||
301 DFIGMSQTDLSLSKVVKHSFVEVNEEGTEAAAAATAAIMMRCARFVPRFC 350
351 ADHPFLFFIQHSKTNIGILFCGR 372
|||||
351 ADHPFLFFIQHRKTNIGILFCGR 372

FIG. 62 (CONT. ¹)

[illegible]

```
351 ADHPFLFFIQQR 362
      | | | | | | | | |
351 ADHPFLFFIQHR 362
```

FIG. 63 (CONT. 1)

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157 VGYRVPAGSGPSLPPMPSLQEVDCGSPSSSEEEGVPGSRGSPATSPHLGR 206
:|||||
1 IGYRVPAGSGPSLPPMPSLQEVDCGSPSSSEEEGVPGSRGSPATSPHLGR 50

207 RRPLLRMSAAFCSL LAPERQVGRAAAALMQDRHTAAGQLVQDLLTQVRD 256
|||||
51 RRPLLRMSAAFCSL LAPERQVGRAAAALMQDRHTAAGQLVQDLLTQVRD 100

257 GORPQEEGIRQALSRARAMLSAELGPEKLVSPKRLEHVLEKSLHCSVLK 306
|||||
101 GORPQEEGIRQALSRARAMLSAELGPEKLVSPKRLEHVLEKSLHCSVLK 150

307 PLRPILAARLRRRLAADGSLGR LAEGLRLARAQGPAGF GSHLSLPSPVEL 356
|||||
151 PLRPILAARLRRRLAADGSLGR LAEGLRLARAQGPAGF GSHLSLPSPVEL 200

357 EQVRQKLLQLVRTYSPSAQVKRLLQACKLLYMALRTQEGEGSGADGFLPL 406
|||||
201 EQVRQKLLQLVRTYSPSAQVKRLLQACKLLYMALRTQEGEGSGADGFLPL 250

FIG. 64

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407 LSLVLAHCDLPELLLEAEYMSLELLEPSLLTGEGGYLTSLASALLSGL 456
|||||
251 LSLVLAHCDLPELLLEAEYMSLELLEPSLLTGEGGYLTSLASALLSGL 300
457 GQAHTPLSPVQELRRSLSLWEQRRRLPATHCFQ 489
|||||
301 GQAHTPLSPVQELRRSLSLWEQRRRLPATHCFQ 333

FIG. 64 (CONT.¹)

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372 AAGTAAASANGAAIKKLSGPLISDFFAKRKRSAPEKSSGVDVPAPCPSPSA 421
|||||
251 AAGTAAASANGAAIKKLSGPLISDFFAKRKRSAPEKSSGVDVPAPCPSPSA 300
422 APGVGSVEQT¹PRKRLR 437
|||||
301 APGVGSVEQT¹PRKRLR 316

FIG. 65 (CONT.¹)

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1 MEPAAGSSMEPSADWLASAAARGLVEKVRQLLEAGADPNAPNSYGRRPIQ 50
|||||
1 MEPAAGSSMEPSADWLASAAARGRVEEVRLLEAGALPNAPNSYGRRPIQ 50
|||||
51 VMMGSARVAELLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLHRA 100
|||||
51 VMMGSARVAELLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLHRA 100
|||||
101 GARLDVRDAWGRLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAAEG 150
|||||
101 GARLDVRDAWGRLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAAEG 150
151 PS 152
||
151 PS 152

FIG. 66

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```
1 MREENKGMPSGGSGDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRRA 50
  |||||
1 MREENKGMPSGGSGDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRRA 50

51 IQVMMGMSARVAELLLHGAEPNCADPATLTRPVHDAAREGEFDTLVVLH 100
  |||||
51 IQVMMGMSARVAELLLHGAEPNCADPATLTRPVHDAAREGEFDTLVVLH 100

101 RAGARLDVRDVGRLPVDLAEELGHRDVARYLRAAAG 137
  |||||
101 RAGARLDVRDVGRLPVDLAEERCHRDVAGYLRTATG 137
```

FIG. 67

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1 MKHSLNALLIFLIITSAGGSGKGPLDQLEKGGETAQASADPQWEQLNNKNL 50
|||||
1 MKHSLNALLIFLIITSAGGSGKGPLDQLEKGGETAQASADPQWEQLNNKNL 50
.
51 SMPLLPADFHKENTVTNDWIPEGEEDDDYLDLEKIFSEDDDDYIDIVDSLS 100
|||||
51 SMPLLPADFHKENTVTNDWIPEGEEDDDYLDLEKIFSEDDDDYIDIVDSLS 100
.
101 VSPTSDVSAGNILQLFHGKSRIQRLNILNAKFAFNLYRVLKQDVNTFDN 150
|||||
101 VSPTSDVSAGNILQLFHGKSRIQRLNILNAKFAFNLYRVLKQDVNTFDN 150
.
151 IFIAPVGISTAMGMISLGLKGETHEQVHSILHFKDFVNASSKYEITTIHN 200
|||||
151 IFIAPVGISTAMGMISLGLKGETHEQVHSILHFKDFVNASSKYEITTIHN 200
.
201 LFRKLTHRLFRNFGYTLRSVNDLYIQKQFPILLDFKTKVREYFAEAQI 250
|||||
201 LFRKLTHRLFRNFGYTLRSVNDLYIQKQFPILLDFKTKVREYFAEAQI 250

FIG. 68

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```
251 ADFSDPAFISKTNHIMKLTGLIKDALENIDPATQMMILNCIYFKGSWV 300
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 ADFSDPAFISKTNHIMKLTGLIKDALENIDPATQMMILNCIYFKGSWV 300

301 NKFPVEMTHNHNFRNLNEREVKVSMQTKGNFLA..... 334
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 NKFPVEMTHNHNFRNLNEREVKVSMQTKGNFLAANDQELDCDILQLEYV 350

335 .....SCLLFMGRVANPSRS 349
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
451 QATTVTVGFMPLSTQVRFTVDRPFELFLIYEHRTSCLLFMGRVANPSRS 499
```

FIG. 68 (CONT. ¹)

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1 MDPARPLGLSILLFLTEAALGDAAQEPTGNNAEICLLPLDYGPCRALLL 50
|||||
1 MDPARPLGLSILLFLTEAALGDAAQEPTGNNAEICLLPLDYGPCRALLL 50
.
51 RYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQV 100
|||||
51 RYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQV 100
.
101 SVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCA 150
|||||
101 SVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCA 150
.
151 PKK.....KYRTCDAFYTGCGGNDNNFVS 175
|||
151 PKKIPFCYSPKDEGLCSANVTRYFNPRTCDAFYTGCGGNDNNFVS 200
.
176 REDCKRACAKALKKKKKMPKILRFASIRKIRKKQF 210
|||||
201 REDCKRACAKALKKKKKMPKILRFASIRKIRKKQF 235

FIG. 70

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```

1 MIYTMKKVHALWASVCLLLNLAPAPLNADSEEDDEHTIITDTPLPKLM 50
  |||||
1 MIYTMKKVHALWASVCLLLNLAPAPLNADSEEDDEHTIITDTPLPKLM 50

. . .
51 HSFCAFKADDPCKAIMKRFFNIFTRQCEEFIYGGCEGNQRFESLEEC 100
  |||||
51 HSFCAFKADDPCKAIMKRFFNIFTRQCEEFIYGGCEGNQRFESLEEC 100

. . .
101 KKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNNQTKQC 150
  |||||
101 KKMCTRDNANRIIKTTLQQEKPDFCFLEEDPGICRGYITRYFYNNQTKQC 150

. . .
151 ERFKYGGCLGNMNNFETLEECKNICEGPNQFQVDNYGTQLNAVNNSLTP 200
  |||||
151 ERFKYGGCLGNMNNFETLEECKNICEGPNQFQVDNYGTQLNAVNNSLTP 200

201 QSTKVPSLF 209
  |||||
201 QSTKVPSLF 209

```

FIG. 71

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201 KDFTCVHQALKGFTTKGVTSVSQIFHSPVDWRLQLQSKSQEVLSQTSTKAR 250

|||||

201 KDFTCVHQALKGFTTKGVTSVSQIFHS..... 227

.
.
.

351 VFRYCFPEFLKYPDDLAIKRTFVNASRTLYSSSPRVLSNNSDANLELINT 400

|||||

228 PDLAIRDTFVNASRTLYSSSPRVLSNNSDANLELINT 264

401 WVAKNTNKKISRLLDLSPLSDTRLVLLNAIYLSAKWKTTFDPKKTRMEPFH 450

|||||

265 WVAKNTNKKISRLLDLSPLSDTRLVLLNAIYLSAKWKTTFDPRKTRMEPFH 314

451 FKNSVIKVPMMNSKKYPVAHFIDQTLKAKVGQLQLSHNLSLVILVPQNLK 500

|||||

315 FKNSVIKVPMMNSKKYPVAHFIDQTLKAKVGQLQLSHNLSLVILVPQNLK 364

.
.
.

FIG. 72 (CONT. ¹)

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1 MDVLAENGTFALNLLKTLGKDNSKNVFFSPMSMICALAMVYMGAKGNTA 50
|||||
1 MDVLAENGTFALNLLKTLGKDNSKNVFFSPMSMICALAMVYMGAKGNTA 50
51 AQMAQILSFNKS GGGDIHQGFQSLLTEVNKTGTQYLLRVANRLFGEKSC 100
|||||
51 AQMAQILSFNKS GGGDIHQGFQSLLTEVNKTGTQYLLRVANRLFGEKSC 100
101 DFLSSFRDSCQKFYQAEMEELDFISAVEKSRKHINTWVAEKTGKIAELL 150
|||||
101 DFLSSFRDSCQKFYQAEMEELDFISAVEKSRKHINTWVAEKTGKIAELL 150
151 SPGSVDPLTRLVLVNAVYFRGNWDGQFDKENTEERL FKVSKNEEKPVQMM 200
|||||
151 SPGSVDPLTRLVLVNAVYFRGNWDGQFDKENTEERL FKVSKNEEKPVQMM 200
201 FKQSTFKKTYIGEIFTQILVLPYVGKELNMIIMLPDETTDLRTVEKELTY 250
|||||
201 FKQSTFKKTYIGEIFTQILVLPYVGKELNMIIMLPDETTDLRTVEKELTY 250

FIG. 73

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[illegible]

FIG. 73 (CONT. 1)


```

1 MDVLAEANGTFALNLLKTLGKDNSKNVFFSPMSMSCALAMVYMGAKGNTA 50
  |||||
1 MDVLAEANGTFALNLLKTLGKDNSKNVFFSPMSMSCALAMVYMGAKGNTA 50

51 AQMAQILSFENKSGGGDIHQGFQSLLTEVNKTGTQYLLRMANRLFGEKSC 100
  |||||
51 AQMAQILSFENKSGGGDIHQGFQSLLTEVNKTGTQYLLRVANRLFGEKSC 100

101 DFLSSFRDSCQKFYQAEMEELDFISAVEKSRKHINTWVAEKTEGKM 146
  |||||
101 DFLSSFRDSCQKFYQAEMEELDFISAVEKSRKHINTWVAEKTEGKI 146

```

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FIG. 75


```

301 DLRDLVTTLGGALLWLSGHAGTQAQGAARVAAALDDGSALGRFERMLAAQ 350
    |||||
301 DLRDLVTTLGGALLWLSGHAGTQAQGAARVAAALDDGSALGRFERMLAAQ 350
    |||||
351 GVDPGLARALCSGSPAERRQLLPRAREQEEELLAPADGERSGESPSFRLRH 400
    |||||
351 GVDPGLARALCSGSPAERRQLLPRAREQEEELLAPAD..... 386
    |||||
401 PLPFPRPRFPSPRLSAPLPAGTVELVRALPLALVLHELGAGRSAGEPL 450
    |||||
387 .....GTVELVRALPLALVLHELGAGRSAGEPL 415
    |||||
451 RLGVGAEELLVDVGQRLRRGTPWLRVHRDGPALSGPQSRALQEALVLSRA 500
    |||||
416 RLGVGAEELLVDVGQRLRRGTPWLRVHRDGPALSGPQSRALQEALVLSRA 465
    |||||
    501 PFAAPSPFAELVLPQQ 517
    |||||
    466 PFAAPSPFAELVLPQQ 482

```

FIG. 76 (CONT.)¹

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1 MGAPACALALCVAVAIVAGASSESLGTEQVRVVGRAAEVPGPEGQQEQLV 50
|||||
1 MGAPACALALCVAVAIVAGASSESLGTEQVRVVGRAAEVPGPEGQQEQLV 50

51 FGSGDAVELSCPPPGGPMGPTVWVKDGTGLVPSEVLVGPQRLQVLNAS 100
|||||
51 FGSGDAVELSCPPPGGPMGPTVWVKDGTGLVPSEVLVGPQRLQVLNAS 100

101 HEDSGAYSCRQRLTQRVLCHFVSRVTDAPSSGDDEDEAEDTGVDTGA 150
|||||
101 HEDSGAYSCRQRLTQRVLCHFVSRVTDAPSSGDDEDEAEDTGVDTGA 150

151 PYWTRPERMDKLLAVPAANTVFRCPAAGNPTPSISWLKNGREFRGEHR 200
|||||
151 PYWTRPERMDKLLAVPAANTVFRCPAAGNPTPSISWLKNGREFRGEHR 200

201 IGGIKLRHQQWSLVMESVVPSPDRGNVTCVVENKFGSIRQTYTLDVLESP 250
|||||
201 IGGIKLRHQQWSLVMESVVPSPDRGNVTCVVENKFGSIRQTYTLDVLESP 250

251 HRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHVEVNGSKVGP 300
|||||
251 HRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHVEVNGSKVGP 300

FIG. 78

[illegible]

FIG. 78 (CONT. 1)

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1 MDPARPLGLSILLFLTEAALGDAAQEPTGNNAEICLLPLDYGPCRALLL 50
|||||
1 MDPARPLGLSILLFLTEAALGDAAQEPTGNNAEICLLPLDYGPCRALLL 50
.
51 RYYYDRYTQSCRQFLYGGCEGNRNNFYTWEACDDACWRIEKVPKVCRLQV 100
|||||
51 RYYYDRYTQSCRQFLYGGCEGNANNFYTWEACDDACWRIEKVPKVCRLQV 100
.
101 SVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCA 150
|||||
101 SVDDQCEGSTEKYFFNLSSMTCEKFFSGGCHRNRIENRFPDEATCMGFCA 150
.
151 PKKIPSEFCYSPKDEGLCSANVTRYFN 177
|||||
151 PKKIPSEFCYSPKDEGLCSANVTRYFN 177

FIG. 79

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1 MNQLRGKKSCHTGLGRSAGWNIPIGLLYCDLPEPRKPLEKAVANFFSGSC 50
|||||
1 MNQLRGKKSCHTGLGRSAGWNIPIGLLYCDLPEPRKPLEKAVANFFSGSC 50

51 APCADGTDFFQLCQLCPGCGCSTLNQYFGYSGAFKCLKDGAGDVAFVKHS 100
|||||
51 APCADGTDFFQLCQLCPGCGCSTLNQYFGYSGAFKCLKDGAGDVAFVKHS 100

101 TIFENLANKADRDQYELLCLDNTRKPVDEYKDCCHLAQVPSHTVVARSMGG 150
|||||
101 TIFENLANKADRDQYELLCLDNTRKPVDEYKDCCHLAQVPSHTVVARSMGG 150

151 KEDLIWELLNQAQEHFGKDKSKEFQLFSSPHGKDLLFKDSAHGFLKVPPR 200
|||||
151 KEDLIWELLNQAQEHFGKDKSKEFQLFSSPHGKDLLFKDSAHGFLKVPPR 200

201 MDAKMYLGYEYVTAIRNLREGTCPEAPTDECKPVKWCALSHHERLKCDEW 250
|||||
201 MDAKMYLGYEYVTAIRNLREGTCPEAPTDECKPVKWCALSHHERLKCDEW 250

FIG. 80

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251	SVNSVGKIECVSAETTEDCIAKIMNGEADAMSLDGGFVYIAGKCGLVPVL	300
251	SVNSVGKIECVSAETTEDCIAKIMNGEADAMSLDGGFVYIAGKCGLVPVL	300
301	AENYNKSDNCEDTPEAGYFAVAVVKKSASDLTWDNLKGKKSCHTAVGRTA	350
301	AENYNKSDNCEDTPEAGYFAVAVVKKSASDLTWDNLKGKKSCHTAVGRTA	350
351	GWNIPMGLLYNKINH.....CEP	368
351	GWNIPMGLLYNKINHCRFDEFSEGCAPGSKKDSLCKLCMGSGLNLC	400
369	NNKEGYGYGTGAFRCLVEKGDVAFVKHQTVPQNTGGKNPDPWAKNLNEKD	418
401	NNKEGYGYGTGAFRCLVEKGDVAFVKHQTVPQNTGGKNPDPWAKNLNEKD	450
419	YELLCLDGTRKPVVEYANCHLARAPNHAVVTRKDKEACVHKILRQQQHLE	468
451	YELLCLDGTRKPVVEYANCHLARAPNHAVVTRKDKEACVHKILRQQQHLE	500

FIG. 80 (CONT. 1)

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469 GSNVTDCSGNFCLFRSETKDLLFRDDTVCLAKLHNRNTYEKYLGEYVKA 518
|||||
501 GSNVTDCSGNFCLFRSETKDLLFRDDTVCLAKLHNRNTYEKYLGEYVKA 550
|||||
519 VGNLRKCSTSSLLEACTFRRP 539
|||||
551 VGNLRKCSTSSLLEACTFRRP 571

FIG. 80 (CONT. ²)

37 NGFQVDNYGTQLNAVNNSLTPQSTKVPSLFEFHGPSWCLTPADRGLCRAN 86
 |||
 180 NGFQVDNYGTQLNAVNNSLTPQSTKVPSLFEFHGPSWCLTPADRGLCRAN 229
 |||
 87 ENRFYNSVIGKCRPFKYSGCGGNENFTSKQECLRACKKGFIQRISKGG 136
 |||
 230 ENRFYNSVIGKCRPFKYSGCGGNENFTSKQECLRACKKGFIQRISKGG 279
 |||
 137 LIKTKRKRKKQRVKIAEYEEIFVKNM 161
 |||
 280 LIKTKRKRKKQRVKIAEYEEIFVKNM 304
 |||

FIG. 82

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13 RPILTIITLEDSSGNLLGRDSFEVRVCASPRDRPTEE 50
|||||
246 RPILTIITLEDSSGNLLGRDSFEVRVCACPRDRRTEE 283

51 ENFRKKEVLCPELPPGSAKRALPTCTASPPQKKKPLDGEYFTLKIRGRK 100
|||||
284 ENFRKKEVLCPELPPGSAKRALPTCTASPPQKKKPLDGEYFTLKIRGRK 333

101 RFEMFRELNELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVK 150
|||||
334 RFEMFRELNELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVK 383

151 KVGPDSD 157
|||||
384 KVGPDSD 390

FIG. 83


```

1  MGAASGQRGRWPLSPPLMLSLVLLQSPAPALDPGLQPGNFSPDEAG 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MGAASGQRGRWPLSPPLMLSLVLLQSPAPALDPGLQPGNFSPDEAG 50

51 AQLFAESYNSSAEVVMFQSTVASWAHDTNITEENARRQEEAALVSQEF 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 AQLFAESYNSSAEVVMFQSTVASWAHDTNITEENARRQEEAALVSQEF 100

101 VWGKKAKELYESIWQNFTDSKLRRIIGSIRTLGPANLPLAQRQQYNSLLS 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 VWGKKAKELYESIWQNFTDSKLRRIIGSIRTLGPANLPLAQRQQYNSLLS 150

1151 NMSRIYSTGKVCFPNKTATCWSLDPELTNILASSRSYAKLLFAWEGW 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1151 NMSRIYSTGKVCFPNKTATCWSLDPELTNILASSRSYAKLLFAWEGW 200

201 VGIPLKPLYQDEFTAISNEAYRQDDFSDTGAFWRWSWYESPSFEESLE 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 VGIPLKPLYQDEFTAISNEAYRQDDFSDTGAFWRWSWYESPSFEESLE 250

```

FIG. 85

251	QLEPLYNLHAYVRRALHRRYGDKYVNLRCPIPAHLLGDMWAQSWENIYD	300
251	QLEPLYNLHAYVRRALHRRYGDKYVNLRCPIPAHLLGDMWAQSWENIYD	300
301	MVVPFPDKNLDTVSTMVQKGNATHMFRVSEEFFTSGLSPMPPEFWAE	350
301	MVVPFPDKNLDTVSTMVQKGNATHMFRVSEEFFTSGLSPMPPEFWAE	350
351	SMLEKPTDGREVVCHASAWDFYNRKDFRIKQCTRVTMQQLATVHHMGHV	400
351	SMLEKPTDGREVVCHASAWDFYNRKDFRIKQCTRVTMQQLATVHHMGHV	400
401	QYYLQYKDLHVSLLRRGANPGFHEAIGDVLALSVESTPAHLHKIGLLDHVTN	450
401	QYYLQYKDLHVSLLRRGANPGFHEAIGDVLALSVESTPAHLHKIGLLDHVTN	450
451	DIESDINYLKMALEKIAFLPGYLVDOQRWGVFSGRTPPSRYNFDWWYL	500
451	DIESDINYLKMALEKIAFLPGYLVDOQRWGVFSGRTPPSRYNFDWWYL	500

FIG. 85 (CONT.)¹

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501 RTKYQGICPPVARNETHFDAGAKFHIPNVTPYIRYFVSFVLQFQFHQALC 550
|||||
501 RTKYQGICPPVARNETHFDAGAKFHIPNVTPYIRYFVSFVLQFQFHQALC 550
|||||

551 KEAGHQGPLHQCDIYQSAQAGAKLKQVLQAGCSRWPQEVVKDLVGSDALD 600
|||||
551 KEAGHQGPLHQCDIYQSAQAGAKLKQVLQAGCSRWPQEVVKDLVGSDALD 600
|||||

601 AKALLEYFQPVSQWLEEQNRNGEVLGWPNQWRPPLPDNYPEGIDLETD 650
|||||
601 AKALLEYFQPVSQWLEEQNRNGEVLGWPNQWRPPLPDNYPEGIDLETD 650
|||||

651 EAKADRFVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVS 700
|||||
651 EAKADRFVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVS 700
|||||

701 HTLKYGTRAKTFDVSFQNSSIKRIIKKLQNLDRVLPKPKELEEYNQILL 750
|||||
701 HTLKYGTRAKTFDVSFQNSSIKRIIKKLQNLDRVLPKPKELEEYNQILL 750
|||||

751 DMETTSLSNICYTNNGTCMPLEPDLTNMMATSRKYEEELLWAWKSWRDKVG 800
|||||
751 DMETTSLSNICYTNNGTCMPLEPDLTNMMATSRKYEEELLWAWKSWRDKVG 800
|||||

FIG. 85 (CONT. ²)

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801 RAILPFFPKYVEFSNKIAKLNKYTDAGDSWRSLYESDNLEQDLEKLYQEL 850
|||||
801 RAILPFFPKYVEFSNKIAKLNKYTDAGDSWRSLYESDNLEQDLEKLYQEL 850
|||||
851 QPLYNLHAYVRRSLHRHYGSEYINLDGPIPAHLLGNMWAQTWSNIYDLV 900
|||||
851 QPLYNLHAYVRRSLHRHYGSEYINLDGPIPAHLLGNMWAQTWSNIYDLV 900
|||||
901 APFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSGLLLPVPPEFWNKSM 950
|||||
901 APFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSGLLLPVPPEFWNKSM 950
|||||
951 LEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMIGHIQY 1000
|||||
951 LEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMIGHIQY 1000
|||||
1001 FMQYKDLPVTTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTEGSGY 1050
|||||
1001 FMQYKDLPVTTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTEGSGY 1050
|||||

FIG. 85 (CONT.³)

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```

11051 EYDINFLMKMALKIAFIPFSYLIDQWRWRFVFDGSI TKENYNQEWSLRL 1100
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
11051 EYDINFLMKMALKIAFIPFSYLIDQWRWRFVFDGSI TKENYNQEWSLRL 1100

11101 KYQGLCPPVPRSQGDFDPGSKFHVPANVPYVR YFVSFI IQFQFHEALCRA 1150
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
11101 KYQGLCPPVPRSQGDFDPGSKFHVPANVPYVR YFVSFI IQFQFHEALCRA 1150

11151 AGHTGPLHKCDIYQSKEAGKLLADAMKLGYSKPWPPEAMKLITGQP NMSAS 1200
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
11151 AGHTGPLHKCDIYQSKEAGKLLADAMKLGYSKPWPPEAMKLITGQP NMSAS 1200

      . . .
1201 AMMNYFKPLTEWLVTENRRRHGETLGPWEYNWAPNT 1235
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1201 AMMNYFKPLTEWLVTENRRRHGETLGPWEYNWAPNT 1235

```

FIG. 85 (CONT'.⁴)

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1 MTMTLHTKASGMALLHQIQGNELEPLNRPQLKMPMERALGEVYVDNSKPT 50
|||||
1 MTMTLHTKASGMALLHQIQGNELEPLNRPQLKMPMERALGEVYVDNSKPT 50

51 VFNYPEGAAYEFNAAAAAASAPVYGQSGIAYGPGSEAAAFSANSLSGA 100
|||||
51 VFNYPEGAAYEFNAAAAAASAPVYGQSGIAYGPGSEAAAFSANSLSGA 100

101 FPQLNSVSPSPMLLLHPPPPQLSPFLHPHGQQVPYYLENEPSAYAVRDTGP 150
|||||
101 FPQLNSVSPSPMLLLHPPPPQLSPFLHPHGQQVPYYLENEPSAYAVRDTGP 150

151 PAFYRSNSDNRRQNGRERLSSSNEKGNMIMESAKETRYCAVCNDYASGYH 200
|||||
151 PAFYRSNSDNRRQNGRERLSSSNEKGNMIMESAKETRYCAVCNDYASGYH 200

201 YGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRRKSCQACRLRKCY 250
|||||
201 YGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRRKSCQACRLRKCY 250

FIG. 86

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FIG. 86 (Cont.¹)

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```

1 MATLLRSKLTNVATSVSNKSOAKVSGMFARMGFQAATDEEAVGFAHCDDL 50
  |||||
1 MATLLRSKLTNVATSVSNKSOAKVSGMFARMGFQAATDEEAVGFAHCDDL 50

51 DFEHRQGLQMDILKSEGEPCGDEGAEPVEGDHYQRGGAPLPPSGSKDQ 100
  |||||
51 DFEHRQGLQMDILKSEGEPCGDEGAEPVEGDHYQRGGAPLPPSGSKDQ 100

101 AVGAGGEFFGGHDKPKITAEAGWNVTNAIQGMFVLGLPYAILHGGYLGFL 150
  |||||
101 AVGAGGEFFGGHDKPKITAEAGWNVTNAIQGMFVLGLPYAILHGGYLGFL 150

151 LIIFAAVVCCYTGKILIACLYEENEDGEVVRVDRDSYVAIANACCAPRFFT 200
  |||||
151 LIIFAAVVCCYTGKILIACLYEENEDGEVVRVDRDSYVAIANACCAPRFFT 200

201 LGGRVVNVVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIITAV 250
  |||||
201 LGGRVVNVVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIITAV 250

```

FIG. 87

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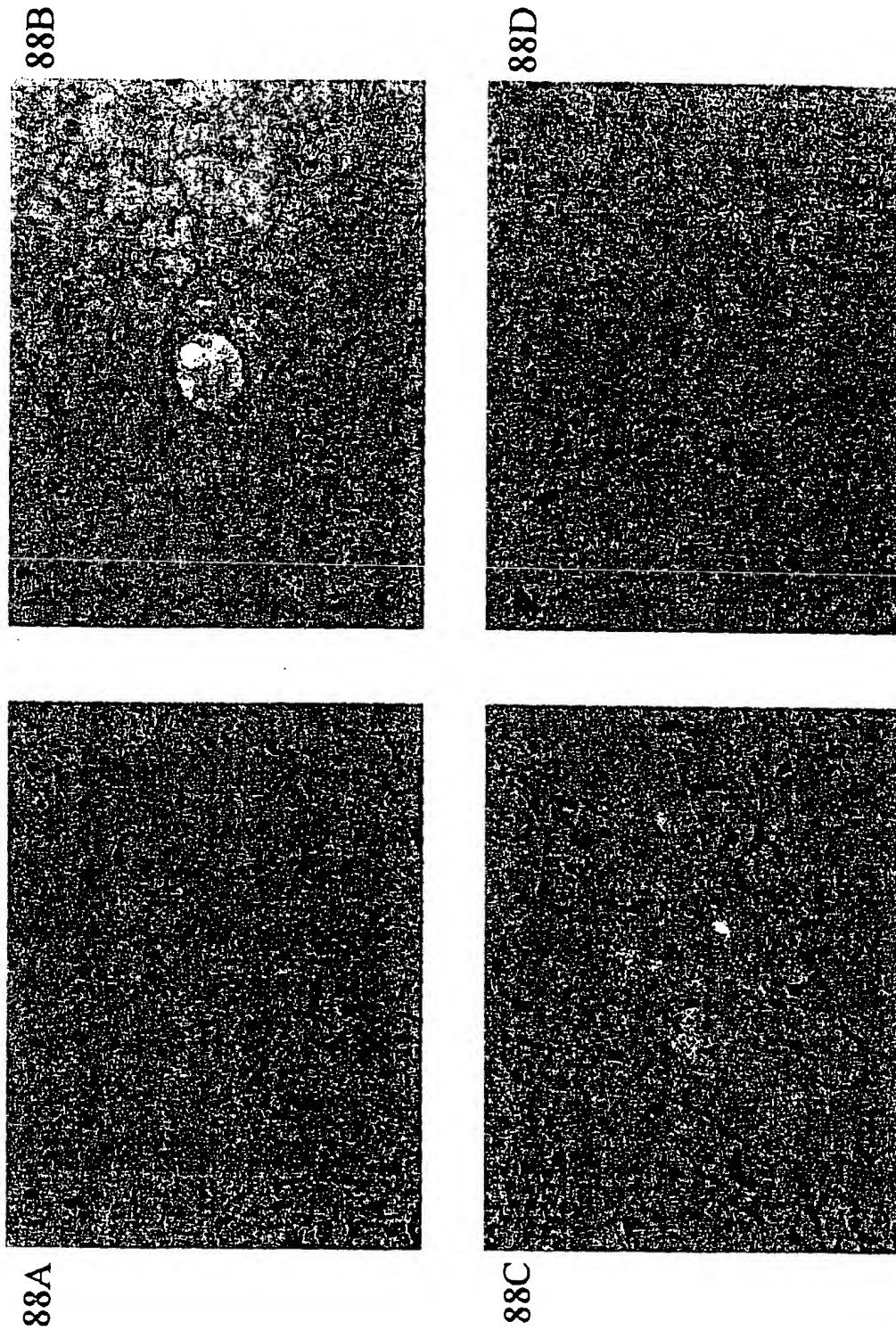
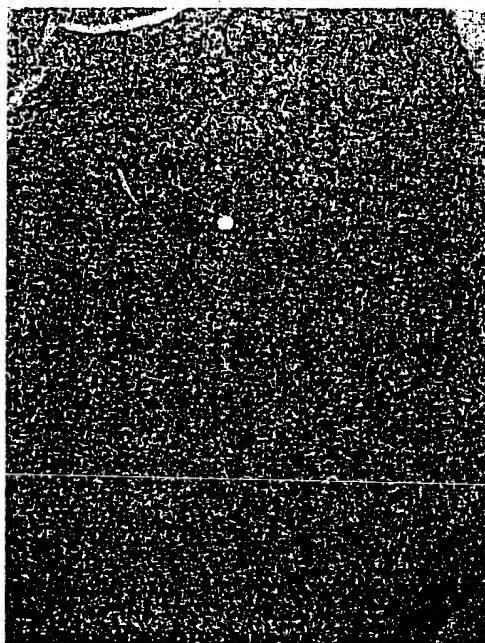
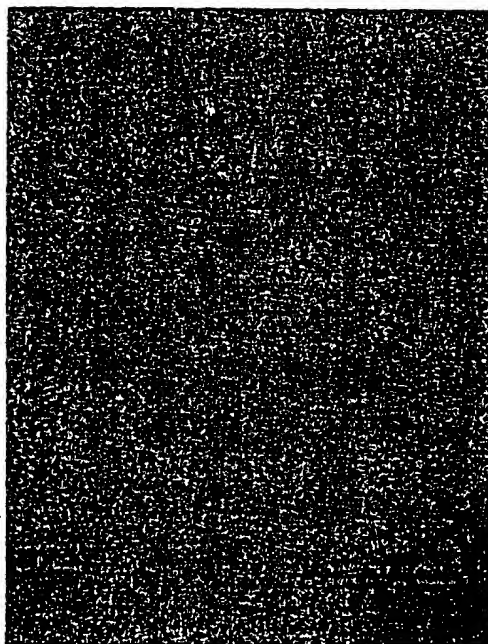


FIG. 88

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89B



89A

FIG. 89

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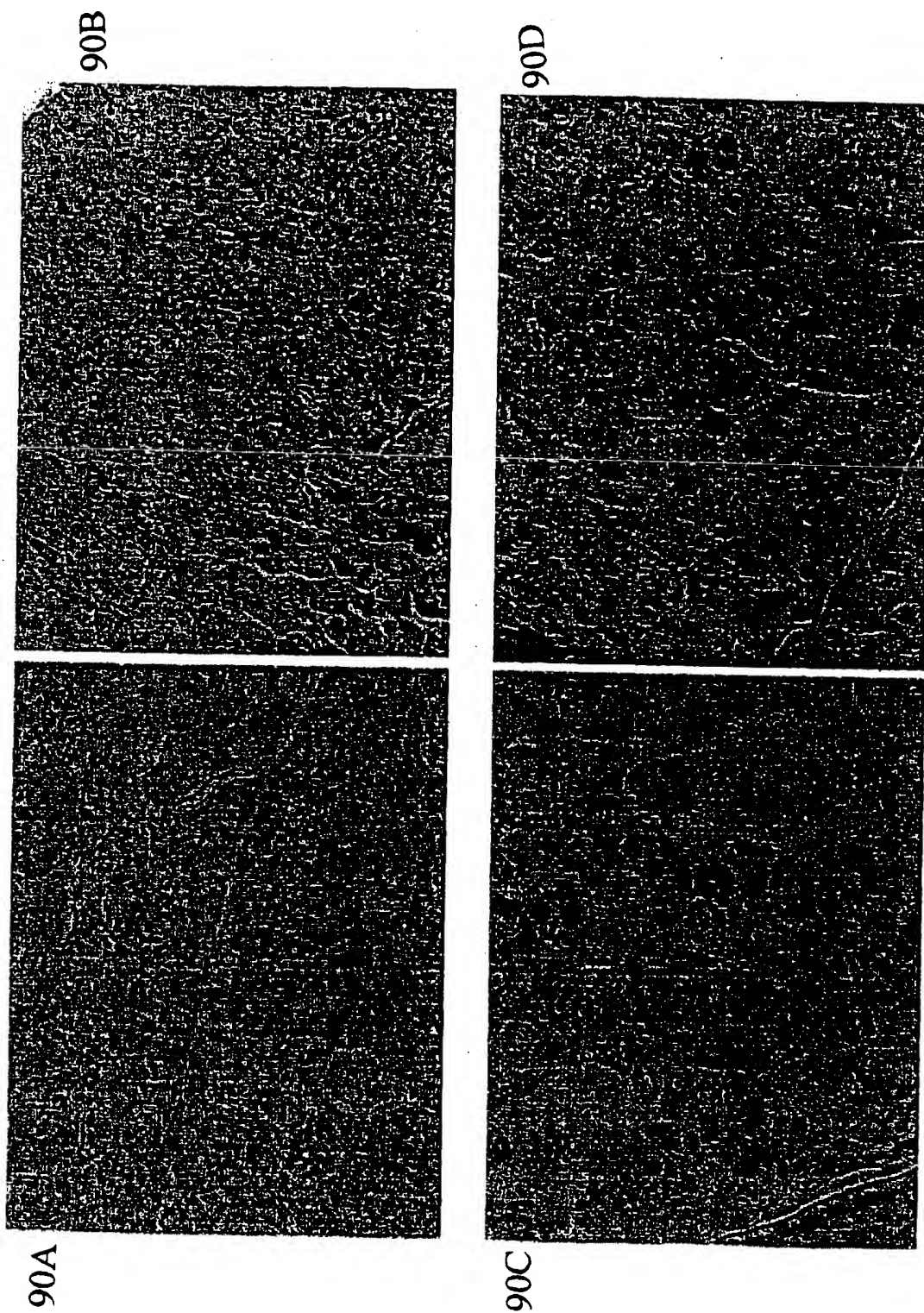


FIG. 90

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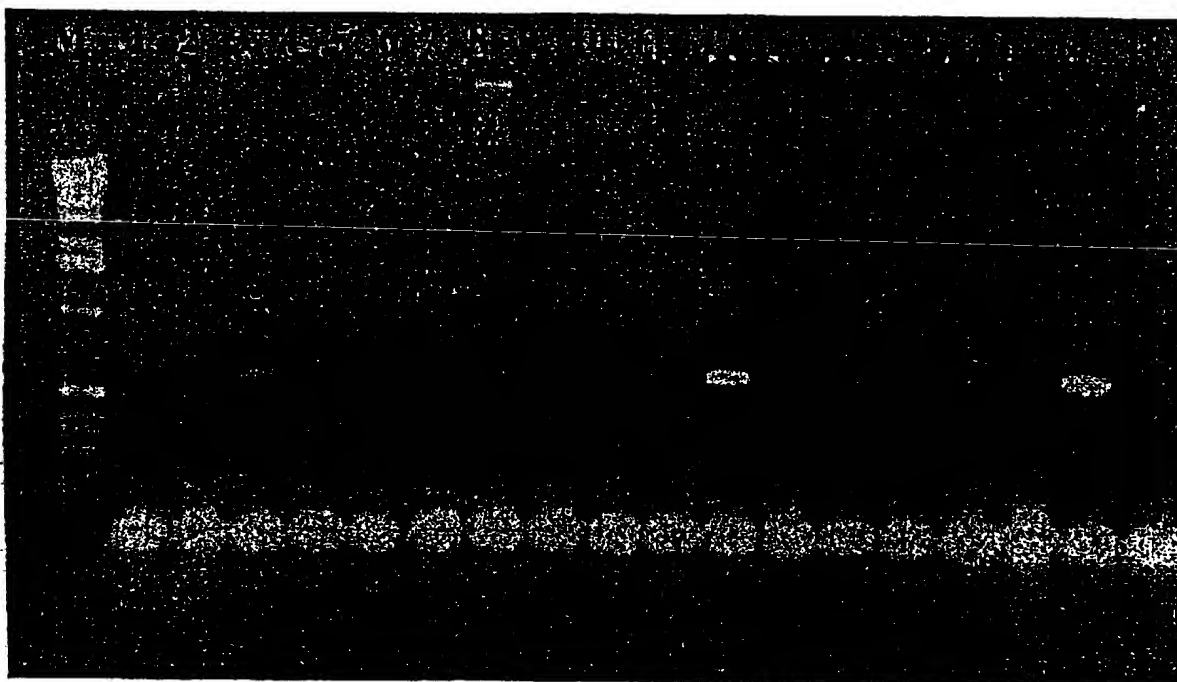
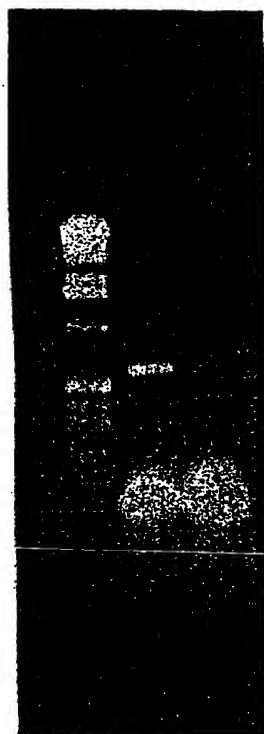


FIG. 91A

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Liver RT+
Liver RT-
Skin RT+
Skin RT-
Thyroid RT+
Thyroid RT-
Bone marrow
RT+
Bone marrow RT-
Salivary gland
RT+
Salivary gland
RT-
Lung RT+
Lung RT-
Heart RT+
Heart RT-
Thymus RT+
Thymus RT-
Spleen RT+
Spleen RT-
Brain RT+
Brain RT-

FIG. 91B

SEQUENCE LISTING

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<151> 1999-11-17

<150> IL133455

<151> 1999-12-10

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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ggcagtgctc cccaccctga gcggaggccc aatggctatg ccctggggct ggtgagtggg 1560
gggagtggcc aagagtccca ggggaacacg ggcctcccag acgtggagct ccttagccat 1620
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gcaggagtgt cctgatgatt catggagttt gcccttctct aagggaagga gatctttatc 1740
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<213> Homo sapiens

<400> 7

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<211> 1700

<212> DNA

<213> Homo sapiens

<400> 8

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<210> 9

<211> 1104

<212> DNA

<213> Homo sapiens

<400> 9

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<210> 10

<211> 967

<212> DNA

<213> Homo sapiens

<400> 10

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<210> 11

<211> 948

<212> DNA

<213> Homo sapiens

<400> 11

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<210> 12

<211> 703

<212> DNA

<213> Homo sapiens

<400> 12

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<210> 13

<211> 2468

<212> DNA

<213> Homo sapiens

<400> 13

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<210> 14

<211> 1850

<212> DNA

<213> Homo sapiens

<400> 14

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<210> 15

<211> 1771

<212> DNA

<213> Homo sapiens

<400> 15

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<210> 16

<211> 1750

<212> DNA

<213> Homo sapiens

<400> 16

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<210> 17

<211> 2101

<212> DNA

<213> Homo sapiens

<400> 17

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<211> 2339

<212> DNA

<213> Homo sapiens

<400> 18

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<210> 19

<211> 1982

<212> DNA

<213> Homo sapiens

<400> 19

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<210> 20

<211> 1804

<212> DNA

<213> Homo sapiens

<400> 20

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<211> 682

<212> DNA

<213> Homo sapiens

<400> 21

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<210> 22

<211> 1349

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 953

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 24

<211> 498

<212> DNA

<213> Homo sapiens

<400> 24

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<213> Homo sapiens

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<400> 27

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<400> 29

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<211> 1679

<212> DNA

<213> Homo sapiens

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<211> 2410

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 1550

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 1922

<212> DNA

<213> Homo sapiens

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<211> 1208

<212> DNA

<213> Homo sapiens

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<211> 1194

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<213> Mouse

<400> 52

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<213> Mouse

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<211> 3058

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<211> 4563

<212> DNA

<213> Homo sapiens

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<210> 58

<211> 1630

<212> DNA

<213> Homo sapiens

<400> 58

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<210> 59

<211> 1551

<212> DNA

<213> Homo sapiens

<400> 59

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<210> 60

<211> 732

<212> DNA

<213> Homo sapiens

<400> 60

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<210> 61

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 61

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<210> 62

<211> 1410

<212> DNA

<213> Homo sapiens

<400> 62

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<210> 63

<211> 1324

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 2235

<212> DNA

<213> Homo sapiens

<400> 64

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<211> 1643

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<213> Homo sapiens

<400> 65

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<211> 722

<212> DNA

<213> Homo sapiens

<400> 66

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<210> 67

<211> 1008

<212> DNA

<213> Homo sapiens

<400> 67

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<210> 68

<211> 1738

<212> DNA

<213> Homo sapiens

<400> 68

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<210> 69

<211> 2308

<212> DNA

<213> Homo sapiens

<400> 69

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<211> 2110

<212> DNA

<213> Homo sapiens

<400> 70

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<211> 1091

<212> DNA

<213> Homo sapiens

<400> 71

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<210> 72

<211> 2267

<212> DNA

<213> Homo sapiens

<400> 72

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<211> 1302

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 868

<212> DNA

<213> Homo sapiens

<400> 74

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<210> 75
 <211> 695
 <212> DNA
 <213> Homo sapiens

<400> 75

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<210> 76
 <211> 3294
 <212> DNA
 <213> Homo sapiens

<400> 76

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<210> 77

<211> 902

<212> DNA

<213> Homo sapiens

<400> 77

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<210> 78

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 78

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<211> 1057

<212> DNA

<213> Homo sapiens

<400> 79

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<210> 80

<211> 2256

<212> DNA

<213> Homo sapiens

<400> 80

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<212> DNA

<213> Homo sapiens

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<213> Mouse

<400> 83

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<210> 84

<211> 969

<212> DNA

<213> Mouse

<400> 84

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969

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<211> 3939

<212> DNA

<213> Mouse

<400> 85

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<211> 1470

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<213> Mouse

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1470

<210> 87

<211> 1723

<212> DNA

<213> Mouse

<400> 87

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<210> 88

<211> 401

<212> PRT

<213> Homo sapiens

<400> 88

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Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
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Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
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145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
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180 185 190

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195 200 205

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr
210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Pro Leu His Ile
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275 280 285

Arg Lys Ile Ile Arg Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys
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305 310 315 320

Glu Gln Val Ser Leu Arg Leu Asn Gly His Pro Pro Gly Val Trp Ala
325 330 335

Asn Gly Ser Ala Pro His Pro Glu Arg Arg Pro Asn Gly Tyr Ala Leu
340 345 350

Gly Leu Val Ser Gly Gly Ser Ala Gln Glu Ser Gln Gly Asn Thr Gly
355 360 365

Leu Pro Asp Val Glu Leu Leu Ser His Glu Leu Lys Gly Val Cys Pro
370 375 380

Glu Pro Pro Gly Leu Asp Asp Pro Leu Ala Gln Asp Gly Ala Gly Val
385 390 395 400

Ser

<210> 89
 <211> 682
 <212> PRT
 <213> Homo sapiens

<400> 89

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Met Pro Arg Tyr Gly Ala Ser Leu Arg Gln Ser Cys Pro Arg Ser Gly
 1           5           10           15

Arg Glu Gln Gly Gln Asp Gly Thr Ala Gly Ala Pro Gly Leu Leu Trp
           20           25           30

Met Gly Leu Val Leu Ala Leu Ala Leu Ala Leu Ala Leu Ser
      35           40           45

Asp Ser Arg Val Leu Trp Ala Pro Ala Glu Ala His Pro Leu Ser Pro
 50           55           60

Gln Gly His Pro Ala Arg Leu His Arg Ile Val Pro Arg Leu Arg Asp
 65           70           75           80

Val Phe Gly Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys Gly Leu Phe
           85           90           95

Thr Ala Ile Asn Leu Gly Leu Lys Lys Glu Pro Asn Val Ala Arg Val
      100           105           110

Gly Ser Val Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile Ala Pro Pro
      115           120           125

Ala Val Cys Gln Ser Ile Val His Leu Phe Glu Asp Asp Met Val Glu
      130           135           140

Val Trp Arg Arg Ser Val Leu Ser Pro Ser Glu Ala Cys Gly Leu Leu
 145           150           155           160

Leu Gly Ser Thr Cys Gly His Trp Asp Ile Phe Ser Ser Trp Asn Ile
      165           170           175

Ser Leu Pro Thr Val Pro Lys Pro Pro Pro Lys Pro Pro Ser Pro Pro
      180           185           190

Ala Pro Gly Ala Pro Val Ser Arg Ile Leu Phe Leu Thr Asp Leu His
      195           200           205

Trp Asp His Asp Tyr Leu Glu Gly Thr Asp Pro Asp Cys Ala Asp Pro
 210           215           220

Leu Cys Cys Arg Arg Gly Ser Gly Leu Pro Pro Ala Ser Arg Pro Gly
 225           230           235           240

Ala Gly Tyr Trp Gly Glu Tyr Ser Lys Cys Asp Leu Pro Leu Arg Thr
      245           250           255

Leu Glu Ser Leu Leu Ser Gly Leu Gly Pro Ala Gly Pro Phe Asp Met
      260           265           270

Val Tyr Trp Thr Gly Asp Ile Pro Ala His Asp Val Trp His Gln Thr

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275					280					285					
Arg	Gln	Asp	Gln	Leu	Arg	Ala	Leu	Thr	Thr	Val	Thr	Ala	Leu	Val	Arg
290					295					300					
Lys	Phe	Leu	Gly	Pro	Val	Pro	Val	Tyr	Pro	Ala	Val	Gly	Asn	His	Glu
305					310					315					320
Ser	Thr	Pro	Val	Asn	Ser	Phe	Pro	Pro	Pro	Phe	Ile	Glu	Gly	Asn	His
				325					330					335	
Ser	Ser	Arg	Trp	Leu	Tyr	Glu	Ala	Met	Ala	Lys	Ala	Trp	Glu	Pro	Trp
			340					345					350		
Leu	Pro	Ala	Glu	Ala	Leu	Arg	Thr	Leu	Arg	Ile	Gly	Gly	Phe	Tyr	Ala
		355					360					365			
Leu	Ser	Pro	Tyr	Pro	Gly	Leu	Arg	Leu	Ile	Ser	Leu	Asn	Met	Asn	Phe
	370					375					380				
Cys	Ser	Arg	Glu	Asn	Phe	Trp	Leu	Leu	Ile	Asn	Ser	Thr	Asp	Pro	Ala
385					390					395					400
Gly	Gln	Leu	Gln	Trp	Leu	Val	Gly	Glu	Leu	Gln	Ala	Ala	Glu	Asp	Arg
				405					410					415	
Gly	Asp	Lys	Val	His	Ile	Ile	Gly	His	Ile	Pro	Pro	Gly	His	Cys	Leu
			420					425					430		
Lys	Ser	Trp	Ser	Trp	Asn	Tyr	Tyr	Arg	Ile	Val	Ala	Arg	Tyr	Glu	Asn
			435				440					445			
Thr	Leu	Ala	Ala	Gln	Phe	Phe	Gly	His	Thr	His	Val	Asp	Glu	Phe	Glu
	450					455					460				
Val	Phe	Tyr	Asp	Glu	Glu	Thr	Leu	Ser	Arg	Pro	Leu	Ala	Val	Ala	Phe
465					470					475					480
Leu	Ala	Pro	Ser	Ala	Thr	Thr	Tyr	Ile	Gly	Leu	Asn	Pro	Leu	Val	Ser
				485					490					495	
Glu	Ala	Glu	Gly	Ser	Leu	Pro	Tyr	Pro	Gly	Val	Gly	Gly	Ile	Gly	Glu
			500					505					510		
Gly	Gly	Trp	Ser	Gln	Ser	Leu	Gln	Ser	Met	Gly	Arg	Met	Cys	Gly	Pro
			515				520					525			
Ser	Leu	Glu	Leu	Pro	Leu	Leu	Leu	Ala	Pro	Pro	Val	Ser	Pro	Thr	Ser
	530					535					540				
Leu	Ala	Gly	Tyr	Arg	Val	Tyr	Gln	Ile	Asp	Gly	Asn	Tyr	Ser	Gly	Ser
545					550					555					560
Ser	His	Val	Val	Leu	Asp	His	Glu	Thr	Tyr	Ile	Leu	Asn	Leu	Thr	Gln
				565					570					575	
Ala	Asn	Ile	Pro	Gly	Ala	Ile	Pro	His	Trp	Gln	Leu	Leu	Tyr	Arg	Ala
			580					585					590		
Arg	Glu	Thr	Tyr	Gly	Leu	Pro	Asn	Thr	Leu	Pro	Thr	Ala	Trp	His	Asn
	595						600					605			

Leu Val Tyr Arg Met Arg Gly Asp Met Gln Leu Phe Gln Thr Phe Trp
610 615 620

Phe Leu Tyr His Lys Gly His Pro Pro Ser Glu Pro Cys Gly Thr Pro
625 630 635 640

Cys Arg Leu Ala Thr Leu Cys Ala Gln Leu Ser Ala Arg Ala Asp Ser
645 650 655

Pro Ala Leu Cys Arg His Leu Met Pro Asp Gly Ser Leu Pro Glu Ala
660 665 670

Gln Ser Leu Trp Pro Arg Pro Leu Phe Cys
675 680

<210> 90

<211> 515

<212> PRT

<213> Homo sapiens

<400> 90

Leu Leu Leu Leu Gly Phe Leu Leu Val Ser Leu Glu Ser Thr Leu Ser
1 5 10 15

Ile Pro Pro Trp Glu Ala Pro Lys Glu His Lys Tyr Lys Ala Glu Glu
20 25 30

His Thr Val Val Leu Thr Val Thr Gly Glu Pro Cys His Phe Pro Phe
35 40 45

Gln Tyr His Arg Gln Leu Tyr His Lys Cys Thr His Lys Gly Arg Pro
50 55 60

Gly Pro Gln Pro Trp Cys Ala Thr Thr Pro Asn Phe Asp Gln Asp Gln
65 70 75 80

Arg Trp Gly Tyr Cys Leu Glu Pro Lys Lys Val Lys Asp His Cys Ser
85 90 95

Lys His Ser Pro Cys Gln Lys Gly Gly Thr Cys Val Asn Met Pro Ser
100 105 110

Gly Pro His Cys Leu Cys Pro Gln His Leu Thr Gly Asn His Cys Gln
115 120 125

Lys Glu Lys Cys Phe Glu Pro Gln Leu Leu Arg Phe Phe His Lys Asn
130 135 140

Glu Ile Trp Tyr Arg Thr Glu Gln Ala Ala Val Ala Arg Cys Gln Cys
145 150 155 160

Lys Gly Pro Asp Ala His Cys Gln Arg Leu Ala Ser Gln Ala Cys Arg
165 170 175

Thr Asn Pro Cys Leu His Gly Gly Arg Cys Leu Glu Val Glu Gly His
180 185 190

Arg Leu Cys His Cys Pro Val Gly Tyr Thr Gly Pro Phe Cys Asp Val
195 200 205

Asp Thr Lys Ala Ser Cys Tyr Asp Gly Arg Gly Leu Ser Tyr Arg Gly
 210 215 220
 Leu Ala Arg Thr Thr Leu Ser Gly Ala Pro Cys Gln Pro Trp Ala Ser
 225 230 235 240
 Glu Ala Thr Tyr Arg Asn Val Thr Ala Glu Gln Ala Arg Asn Trp Gly
 245 250 255
 Leu Gly Gly His Ala Phe Cys Arg Asn Pro Asp Asn Asp Ile Arg Pro
 260 265 270
 Trp Cys Phe Val Leu Asn Arg Asp Arg Leu Ser Trp Glu Tyr Cys Asp
 275 280 285
 Leu Ala Gln Cys Gln Thr Pro Thr Gln Ala Ala Pro Pro Thr Pro Val
 290 295 300
 Ser Pro Arg Leu His Val Pro Leu Met Pro Ala Gln Pro Ala Pro Pro
 305 310 315 320
 Lys Pro Gln Pro Thr Thr Arg Thr Pro Pro Gln Ser Gln Thr Pro Gly
 325 330 335
 Ala Leu Pro Ala Lys Arg Glu Gln Pro Pro Ser Leu Thr Arg Asn Gly
 340 345 350
 Pro Leu Ser Cys Gly Gln Arg Leu Arg Lys Ser Leu Ser Ser Met Thr
 355 360 365
 Arg Val Val Gly Gly Leu Val Ala Leu Arg Gly Ala His Pro Tyr Ile
 370 375 380
 Ala Ala Leu Tyr Trp Gly His Ser Phe Cys Ala Gly Ser Leu Ile Ala
 385 390 395 400
 Pro Cys Trp Val Leu Thr Ala Ala His Cys Leu Gln Asp Arg Pro Ala
 405 410 415
 Pro Glu Asp Leu Thr Val Val Leu Gly Gln Glu Arg Arg Asn His Ser
 420 425 430
 Cys Glu Pro Cys Gln Thr Leu Ala Val Arg Ser Tyr Arg Leu His Glu
 435 440 445
 Ala Phe Ser Pro Val Ser Tyr Gln His Asp Leu Ala Leu Leu Arg Leu
 450 455 460
 Gln Glu Asp Ala Asp Gly Ser Cys Ala Leu Leu Ser Pro Tyr Val Gln
 465 470 475 480
 Pro Val Cys Leu Pro Ser Gly Ala Ala Arg Pro Ser Glu Thr Thr Leu
 485 490 495
 Cys Gln Val Ala Gly Trp Gly His Gln Phe Glu Ala Ser Leu Pro Met
 500 505 510
 Lys Leu Asn
 515

<210> 91
 <211> 775
 <212> PRT
 <213> Homo sapiens

<400> 91

Met Ala Arg Leu Gly Asn Cys Ser Leu Thr Trp Ala Ala Leu Ile Ile
 1 5 10 15

Leu Leu Leu Pro Gly Ser Leu Glu Glu Cys Gly His Ile Ser Val Ser
 20 25 30

Ala Pro Ile Val His Leu Gly Asp Pro Ile Thr Ala Ser Cys Ile Ile
 35 40 45

Lys Gln Asn Cys Ser His Leu Asp Pro Glu Pro Gln Ile Leu Trp Arg
 50 55 60

Leu Gly Ala Glu Leu Gln Pro Gly Gly Arg Gln Gln Arg Leu Ser Asp
 65 70 75 80

Gly Thr Gln Glu Ser Ile Ile Thr Leu Pro His Leu Asn His Thr Gln
 85 90 95

Ala Phe Leu Ser Cys Cys Leu Asn Trp Gly Asn Ser Leu Gln Ile Leu
 100 105 110

Asp Gln Val Glu Leu Arg Ala Gly Tyr Pro Pro Ala Ile Pro His Asn
 115 120 125

Leu Ser Cys Leu Met Asn Leu Thr Thr Ser Ser Leu Ile Cys Gln Trp
 130 135 140

Glu Pro Gly Pro Glu Thr His Leu Pro Thr Ser Phe Thr Leu Lys Ser
 145 150 155 160

Phe Lys Ser Arg Gly Asn Cys Gln Thr Gln Gly Asp Ser Ile Leu Asp
 165 170 175

Cys Val Pro Lys Asp Gly Gln Ser His Cys Cys Ile Pro Arg Lys His
 180 185 190

Leu Leu Leu Tyr Gln Asn Met Gly Ile Trp Val Gln Ala Glu Asn Ala
 195 200 205

Leu Gly Thr Ser Met Ser Pro Gln Leu Cys Leu Asp Pro Met Asp Val
 210 215 220

Val Lys Leu Glu Pro Pro Met Leu Arg Thr Met Asp Pro Ser Pro Glu
 225 230 235 240

Ala Ala Pro Pro Gln Ala Gly Cys Leu Gln Leu Cys Trp Glu Pro Trp
 245 250 255

Gln Pro Gly Leu His Ile Asn Gln Lys Cys Glu Leu Arg His Lys Pro
 260 265 270

Gln Arg Gly Glu Ala Ser Trp Ala Leu Val Gly Pro Leu Pro Leu Glu
 275 280 285

Ala	Leu	Gln	Tyr	Glu	Leu	Cys	Gly	Leu	Leu	Pro	Ala	Thr	Ala	Tyr	Thr	290	295	300	
Leu	Gln	Ile	Arg	Cys	Ile	Arg	Trp	Pro	Leu	Pro	Gly	His	Trp	Ser	Asp	305	310	315	320
Gly	Ala	Ile	Leu	Pro	Leu	Cys	Asn	Thr	Thr	Glu	Leu	Ser	Cys	Thr	Phe	325	330	335	
His	Leu	Pro	Ser	Glu	Ala	Gln	Glu	Val	Ala	Leu	Val	Ala	Tyr	Asn	Ser	340	345	350	
Ala	Gly	Thr	Ser	Arg	Pro	Thr	Pro	Val	Val	Phe	Ser	Glu	Ser	Arg	Gly	355	360	365	
Pro	Ala	Leu	Thr	Arg	Leu	His	Ala	Met	Ala	Arg	Asp	Pro	His	Ser	Leu	370	375	380	
Trp	Val	Gly	Trp	Glu	Pro	Pro	Asn	Pro	Trp	Pro	Gln	Gly	Tyr	Val	Ile	385	390	395	400
Glu	Trp	Gly	Leu	Gly	Pro	Pro	Ser	Ala	Ser	Asn	Ser	Asn	Lys	Thr	Trp	405	410	415	
Arg	Met	Glu	Gln	Asn	Gly	Arg	Ala	Thr	Gly	Phe	Leu	Leu	Lys	Glu	Asn	420	425	430	
Ile	Arg	Pro	Phe	Gln	Leu	Tyr	Glu	Ile	Ile	Val	Thr	Pro	Leu	Tyr	Gln	435	440	445	
Asp	Thr	Met	Gly	Pro	Ser	Gln	His	Val	Tyr	Ala	Tyr	Ser	Gln	Glu	Met	450	455	460	
Ala	Pro	Ser	His	Ala	Pro	Glu	Leu	His	Leu	Lys	His	Ile	Gly	Lys	Thr	465	470	475	480
Trp	Ala	Gln	Leu	Glu	Trp	Val	Pro	Glu	Pro	Pro	Glu	Leu	Gly	Lys	Ser	485	490	495	
Pro	Leu	Thr	His	Tyr	Thr	Ile	Phe	Trp	Thr	Asn	Ala	Gln	Asn	Gln	Ser	500	505	510	
Phe	Ser	Ala	Ile	Leu	Asn	Ala	Ser	Ser	Arg	Gly	Phe	Val	Leu	His	Gly	515	520	525	
Leu	Glu	Pro	Ala	Ser	Leu	Tyr	His	Ile	His	Leu	Met	Ala	Ala	Ser	Gln	530	535	540	
Ala	Gly	Ala	Thr	Asn	Ser	Thr	Val	Leu	Thr	Leu	Met	Thr	Leu	Thr	Pro	545	550	555	560
Glu	Gly	Ser	Glu	Leu	His	Ile	Ile	Leu	Gly	Leu	Phe	Gly	Leu	Leu	Leu	565	570	575	
Leu	Leu	Thr	Cys	Leu	Cys	Gly	Thr	Ala	Trp	Leu	Cys	Cys	Ser	Pro	Asn	580	585	590	
Arg	Lys	Asn	Pro	Leu	Trp	Pro	Ser	Val	Pro	Asp	Pro	Ala	His	Ser	Ser	595	600	605	
Leu	Gly	Ser	Trp	Val	Pro	Thr	Ile	Met	Glu	Glu	Asp	Ala	Phe	Gln	Leu				

610	615	620
Pro Gly Leu Gly Thr	Pro Pro Ile Thr Lys	Leu Thr Val Leu Glu Glu
625	630	635 640
Asp Glu Lys Lys Pro Val Pro Trp Glu Ser His Asn Ser Ser Glu Thr	645 650	655
Cys Gly Leu Pro Thr Leu Val Gln Thr Tyr Val Leu Gln Gly Asp Pro	660 665	670
Arg Ala Val Ser Thr Gln Pro Gln Ser Gln Ser Gly Thr Ser Asp Gln	675 680	685
Val Leu Tyr Gly Gln Leu Leu Gly Ser Pro Thr Ser Pro Gly Pro Gly	690 695	700
His Tyr Leu Arg Cys Asp Ser Thr Gln Pro Leu Leu Ala Gly Leu Thr	705 710	715 720
Pro Ser Pro Lys Ser Tyr Glu Asn Leu Trp Phe Gln Ala Ser Pro Leu	725 730	735
Gly Thr Leu Val Thr Pro Ala Pro Ser Gln Glu Asp Asp Cys Val Phe	740 745	750
Gly Pro Leu Leu Asn Phe Pro Leu Leu Gln Gly Ile Arg Val His Gly	755 760	765
Met Glu Ala Leu Gly Ser Phe	770 775	

<210> 92
 <211> 873
 <212> PRT
 <213> Homo sapiens

<400> 92

Met Ala Arg Leu Gly Asn Cys Ser Leu Thr Trp Ala Ala Leu Ile Ile	1 5 10 15
Leu Leu Leu Pro Gly Ser Leu Glu Glu Cys Gly His Ile Ser Val Ser	20 25 30
Ala Pro Ile Val His Leu Gly Asp Pro Ile Thr Ala Ser Cys Ile Ile	35 40 45
Lys Gln Asn Cys Ser His Leu Asp Pro Glu Pro Gln Ile Leu Trp Arg	50 55 60
Leu Gly Ala Glu Leu Gln Pro Gly Gly Arg Gln Gln Arg Leu Ser Asp	65 70 75 80
Gly Thr Gln Glu Ser Ile Ile Thr Leu Pro His Leu Asn His Thr Gln	85 90 95
Ala Phe Leu Ser Cys Cys Leu Asn Trp Gly Asn Ser Leu Gln Ile Leu	100 105 110
Asp Gln Val Glu Leu Arg Ala Gly Tyr Pro Pro Ala Ile Pro His Asn	

115	120	125
Leu Ser Cys Leu Met Asn Leu Thr Thr Ser Ser Leu Ile Cys Gln Trp		
130	135	140
Glu Pro Gly Pro Glu Thr His Leu Pro Thr Ser Phe Thr Leu Lys Ser		
145	150	155
Phe Lys Ser Arg Gly Asn Cys Gln Thr Gln Gly Asp Ser Ile Leu Asp		
	165	170
		175
Cys Val Pro Lys Asp Gly Gln Ser His Cys Cys Ile Pro Arg Lys His		
	180	185
		190
Leu Leu Leu Tyr Gln Asn Met Gly Ile Trp Val Gln Ala Glu Asn Ala		
	195	200
		205
Leu Gly Thr Ser Met Ser Pro Gln Leu Cys Leu Asp Pro Met Asp Val		
	210	215
		220
Val Lys Leu Glu Pro Pro Met Leu Arg Thr Met Asp Pro Ser Pro Glu		
	225	230
		235
Ala Ala Pro Pro Gln Ala Gly Cys Leu Gln Leu Cys Trp Glu Pro Trp		
	245	250
		255
Gln Pro Gly Leu His Ile Asn Gln Lys Cys Glu Leu Arg His Lys Pro		
	260	265
		270
Gln Arg Gly Glu Ala Ser Trp Ala Leu Val Gly Pro Leu Pro Leu Glu		
	275	280
		285
Ala Leu Gln Tyr Glu Leu Cys Gly Leu Leu Pro Ala Thr Ala Tyr Thr		
	290	295
		300
Leu Gln Ile Arg Cys Ile Arg Trp Pro Leu Pro Gly His Trp Ser Asp		
	305	310
		315
Trp Ser Pro Ser Leu Glu Leu Arg Thr Thr Glu Arg Ala Pro Thr Val		
	325	330
		335
Arg Leu Asp Thr Trp Trp Arg Gln Arg Gln Leu Asp Pro Arg Thr Val		
	340	345
		350
Gln Leu Phe Trp Lys Pro Val Pro Leu Glu Glu Asp Ser Gly Arg Ile		
	355	360
		365
Gln Gly Tyr Val Val Ser Trp Arg Pro Ser Gly Gln Ala Gly Ala Ile		
	370	375
		380
Leu Pro Leu Cys Asn Thr Thr Glu Leu Ser Cys Thr Phe His Leu Pro		
	385	390
		395
Ser Glu Ala Gln Glu Val Ala Leu Val Ala Tyr Asn Ser Ala Gly Thr		
	405	410
		415
Ser Arg Pro Thr Pro Val Val Phe Ser Glu Ser Arg Gly Pro Ala Leu		
	420	425
		430
Thr Arg Leu His Ala Met Ala Arg Asp Pro His Ser Leu Trp Val Gly		
	435	440
		445

Trp Glu Pro Pro Asn Pro Trp Pro Gln Gly Tyr Val Ile Glu Trp Gly
 450 455 460
 Leu Gly Pro Pro Ser Ala Ser Asn Ser Asn Lys Thr Trp Arg Met Glu
 465 470 475 480
 Gln Asn Gly Arg Ala Thr Gly Phe Leu Leu Lys Glu Asn Ile Arg Pro
 485 490 495
 Phe Gln Leu Tyr Glu Ile Ile Val Thr Pro Leu Tyr Gln Asp Thr Met
 500 505 510
 Gly Pro Ser Gln His Val Tyr Ala Tyr Ser Gln Glu Met Ala Pro Ser
 515 520 525
 His Ala Pro Glu Leu His Leu Lys His Ile Gly Lys Thr Trp Ala Gln
 530 535 540
 Leu Glu Trp Val Pro Glu Pro Pro Glu Leu Gly Lys Ser Pro Leu Thr
 545 550 555 560
 His Tyr Thr Ile Phe Trp Thr Asn Ala Gln Asn Gln Ser Phe Cys Glu
 565 570 575
 Ser Xaa Leu Ser Ser Pro Thr Ala Pro Glu Gly Leu Glu Gly Gly Ala
 580 585 590
 Gln Leu Pro Arg Arg Xaa Phe Thr Ile Gln Ala Tyr Ala Asp Arg Thr
 595 600 605
 Pro Leu Pro Ala Ala Ile Leu Asn Ala Ser Ser Arg Gly Phe Val Leu
 610 615 620
 His Gly Leu Glu Pro Ala Ser Leu Tyr His Ile His Leu Met Ala Ala
 625 630 635 640
 Ser Gln Ala Gly Ala Thr Asn Ser Thr Val Leu Thr Leu Met Thr Leu
 645 650 655
 Thr Pro Glu Gly Ser Glu Leu His Ile Ile Leu Gly Leu Phe Gly Leu
 660 665 670
 Leu Leu Leu Leu Thr Cys Leu Cys Gly Thr Ala Trp Leu Cys Cys Ser
 675 680 685
 Pro Asn Arg Lys Asn Pro Leu Trp Pro Ser Val Pro Asp Pro Ala His
 690 695 700
 Ser Ser Leu Gly Ser Trp Val Pro Thr Ile Met Glu Glu Asp Ala Phe
 705 710 715 720
 Gln Leu Pro Gly Leu Gly Thr Pro Pro Ile Thr Lys Leu Thr Val Leu
 725 730 735
 Glu Glu Asp Glu Lys Lys Pro Val Pro Trp Glu Ser His Asn Ser Ser
 740 745 750
 Glu Thr Cys Gly Leu Pro Thr Leu Val Gln Thr Tyr Val Leu Gln Gly
 755 760 765

Asp Pro Arg Ala Val Ser Thr Gln Pro Gln Ser Gln Ser Gly Thr Ser
 770 775 780
 Asp Gln Val Leu Tyr Gly Gln Leu Leu Gly Ser Pro Thr Ser Pro Gly
 785 790 795 800
 Pro Gly His Tyr Leu Arg Cys Asp Ser Thr Gln Pro Leu Leu Ala Gly
 805 810 815
 Leu Thr Pro Ser Pro Lys Ser Tyr Glu Asn Leu Trp Phe Gln Ala Ser
 820 825 830
 Pro Leu Gly Thr Leu Val Thr Pro Ala Pro Ser Gln Glu Asp Asp Cys
 835 840 845
 Val Phe Gly Pro Leu Leu Asn Phe Pro Leu Leu Gln Gly Ile Arg Val
 850 855 860
 His Gly Met Glu Ala Leu Gly Ser Phe
 865 870

<210> 93
 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 93

Met Gln Lys Ile Met His Ile Ser Val Leu Leu Ser Pro Val Leu Trp
 1 5 10 15
 Gly Leu Ile Phe Gly Val Ser Ser Asn Ser Ile Gln Ile Gly Gly Leu
 20 25 30
 Phe Pro Arg Gly Ala Asp Gln Glu Tyr Ser Ala Phe Arg Val Gly Met
 35 40 45
 Val Gln Phe Ser Thr Ser Glu Phe Arg Leu Thr Pro His Ile Asp Asn
 50 55 60
 Leu Glu Val Ala Asn Ser Phe Ala Val Thr Asn Ala Phe Cys Ser Gln
 65 70 75 80
 Phe Ser Arg Gly Val Tyr Ala Ile Phe Gly Phe Tyr Asp Lys Lys Ser
 85 90 95
 Val Asn Thr Ile Thr Ser Phe Cys Gly Thr Leu His Val Ser Phe Ile
 100 105 110
 Thr Pro Ser Phe Pro Thr Asp Gly Thr His Pro Phe Val Ile Gln Met
 115 120 125
 Arg Pro Asp Leu Lys Gly Ala Leu Leu Ser Leu Ile Glu Tyr Tyr Gln
 130 135 140
 Trp Asp Lys Phe Ala Tyr Leu Tyr Asp Ser Asp Arg Gly Leu Ser Thr
 145 150 155 160
 Leu Gln Ala Val Leu Asp Ser Ala Ala Glu Lys Lys Trp Gln Val Thr
 165 170 175

Ala Ile Asn Val Gly Asn Ile Asn Asn Asp Lys Lys Asp Glu Met Tyr
 180 185 190
 Arg Ser Leu Phe Gln Asp Leu Glu Leu Lys Lys Glu Arg Arg Val Ile
 195 200 205
 Leu Asp Cys Glu Arg Asp Lys Val Asn Asp Ile Val Asp Gln Val Ile
 210 215 220
 Thr Ile Gly Lys His Val Lys Gly Tyr His Tyr Ile Ile Ala Asn Leu
 225 230 235 240
 Glu Phe Thr Asp Gly Asp Leu Leu Lys Ile Gln Phe Gly Gly Ala Asn
 245 250 255
 Val Ser Gly Phe Gln Ile Val Asp Tyr Asp Asp Ser Leu Val Ser Lys
 260 265 270
 Phe Ile Glu Arg Trp Ser Thr Leu Glu Glu Lys Glu Tyr Pro Gly Ala
 275 280 285
 His Thr Thr Thr Ile Lys Tyr Thr Ser Ala Leu Thr Tyr Asp Ala Val
 290 295 300
 Gln Val Met Thr Glu Ala Phe Arg Asn Leu Arg Lys Gln Arg Ile Glu
 305 310 315 320
 Ile Ser Arg Arg Gly Asn Ala Gly Asp Cys Leu Ala Asn Pro Ala Val
 325 330 335
 Pro Trp Gly Gln Gly Val Glu Ile Glu Arg Ala Leu Lys Gln Val Gln
 340 345 350
 Val Glu Gly Leu Ser Gly Asn Ile Lys Phe Asp Gln Asn Gly Lys Arg
 355 360 365
 Ile Asn Tyr Thr Ile Asn Ile Met Glu Leu Lys Thr Asn Gly Pro Arg
 370 375 380
 Lys Ile Gly Tyr Trp Ser Glu Val Asp Lys Met Val Val Thr Leu Thr
 385 390 395 400
 Glu Leu Pro Ser Gly Asn Asp Thr Ser Gly Leu Glu Asn Lys Thr Val
 405 410 415
 Val Val Thr Thr Ile Leu Glu Ser Pro Tyr Val Met Met Lys Lys Asn
 420 425 430
 His Glu Met Leu Glu Gly Asn Glu Arg Tyr Glu Gly Tyr Cys Val Asp
 435 440 445
 Leu Ala Ala Glu Ile Ala Lys His Cys Gly Phe Lys Tyr Lys Leu Thr
 450 455 460
 Ile Val Gly Asp Gly Lys Tyr Gly Ala Arg Asp Ala Asp Thr Lys Ile
 465 470 475 480
 Trp Asn Gly Met Val Gly Glu Leu Val Tyr Gly Lys Ala Asp Ile Ala
 485 490 495
 Ile Ala Pro Leu Thr Ile Thr Leu Val Arg Glu Glu Val Ile Asp Phe

500										505					510				
Ser	Lys	Pro	Phe	Met	Ser	Leu	Gly	Ile	Ser	Ile	Met	Ile	Lys	Lys	Pro				
		515					520				525								
Gln	Lys	Ser	Lys	Pro	Gly	Val	Phe	Ser	Phe	Leu	Asp	Pro	Leu	Ala	Tyr				
	530					535					540								
Glu	Ile	Trp	Met	Cys	Ile	Val	Phe	Ala	Tyr	Ile	Gly	Val	Ser	Val	Val				
545					550					555					560				
Leu	Phe	Leu	Val	Ser	Arg	Phe	Ser	Pro	Tyr	Glu	Trp	His	Thr	Glu	Glu				
				565					570					575					
Phe	Glu	Asp	Gly	Arg	Glu	Thr	Gln	Ser	Ser	Glu	Ser	Thr	Asn	Glu	Phe				
			580					585					590						
Gly	Ile	Phe	Asn	Ser	Leu	Trp	Phe	Ser	Leu	Gly	Ala	Phe	Met	Arg	Gln				
		595					600					605							
Gly	Cys	Asp	Ile	Ser	Pro	Arg	Ser	Leu	Ser	Gly	Arg	Ile	Val	Gly	Gly				
	610					615				620									
Val	Trp	Trp	Phe	Phe	Thr	Leu	Ile	Ile	Ile	Ser	Ser	Tyr	Thr	Ala	Asn				
625					630					635					640				
Leu	Ala	Ala	Phe	Leu	Thr	Val	Glu	Arg	Met	Val	Ser	Pro	Ile	Glu	Ser				
				645					650					655					
Ala	Glu	Asp	Leu	Ser	Lys	Gln	Thr	Glu	Ile	Ala	Tyr	Gly	Thr	Leu	Asp				
			660					665					670						
Ser	Gly	Ser	Thr	Lys	Glu	Phe	Phe	Arg	Arg	Ser	Lys	Ile	Ala	Val	Phe				
		675					680					685							
Asp	Lys	Met	Trp	Thr	Tyr	Met	Arg	Ser	Ala	Glu	Pro	Ser	Val	Phe	Val				
	690					695					700								
Arg	Thr	Thr	Ala	Glu	Gly	Val	Ala	Arg	Val	Arg	Lys	Ser	Lys	Gly	Lys				
705					710					715					720				
Tyr	Ala	Tyr	Leu	Leu	Glu	Ser	Thr	Met	Asn	Glu	Tyr	Ile	Glu	Gln	Arg				
			725						730					735					
Lys	Pro	Cys	Asp	Thr	Met	Lys	Val	Gly	Gly	Asn	Leu	Asp	Ser	Lys	Gly				
			740					745					750						
Tyr	Gly	Ile	Ala	Thr	Pro	Lys	Gly	Ser	Ser	Leu	Gly	Thr	Pro	Val	Asn				
		755					760					765							
Leu	Ala	Val	Leu	Lys	Leu	Ser	Glu	Gln	Gly	Val	Leu	Asp	Lys	Leu	Lys				
	770					775					780								
Asn	Lys	Trp	Trp	Tyr	Asp	Lys	Gly	Glu	Xaa	Gly	Xaa	Gly	Glu	Val	Ile				
785					790					795					800				
Pro	Arg	Ser	Ala	Pro	Val	Arg	Lys	Val	Met	Gly	Asn	Ser	Met	Gln	Asn				
				805					810					815					
Lys	Val	Ser	Ser	Ser	Tyr	Ala	Gln	Cys	Gly	His	Ser	Val	His	Pro	Ser				
			820					825					830						

Phe Gln Arg Leu Ser
835

<210> 94
<211> 156
<212> PRT
<213> Homo sapiens

<400> 94
Met Lys Ser Ile Tyr Phe Val Ala Gly Leu Phe Val Met Leu Val Gln
1 5 10 15
Gly Ser Trp Gln Arg Ser Leu Gln Asp Thr Glu Glu Lys Ser Arg Ser
20 25 30
Phe Ser Ala Ser Gln Ala Asp Pro Leu Ser Asp Pro Asp Gln Met Asn
35 40 45
Glu Asp Lys Arg His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys
50 55 60
Tyr Leu Asp Ser Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn
65 70 75 80
Thr Lys Arg Asn Arg Asn Asn Ile Ala Lys Arg His Asp Glu Phe Glu
85 90 95
Arg His Ala Glu Gly Thr Phe Thr Ser Val Ile Phe Pro Glu Glu Val
100 105 110
Ala Ile Val Glu Glu Leu Gly Arg Arg His Ala Asp Gly Ser Phe Ser
115 120 125
Asp Glu Met Asn Thr Ile Ser Asp Asn Leu Ala Ala Arg Asp Phe Ile
130 135 140
Asn Trp Leu Ile Gln Thr Lys Ile Thr Asp Arg Lys
145 150 155

<210> 95
<211> 303
<212> PRT
<213> Homo sapiens

<400> 95
Met Leu Ser Phe Ile Ser Gly Thr Ala Arg Lys Thr Leu His Phe Glu
1 5 10 15
Ile Ser Lys Glu Gly Ser Asp Leu Ser Val Val Glu Arg Ala Glu Val
20 25 30
Trp Leu Phe Leu Lys Val Pro Lys Ala Asn Arg Thr Arg Thr Lys Val
35 40 45
Thr Ile Arg Leu Phe Gln Gln Gln Lys His Pro Gln Gly Ser Leu Asp
50 55 60
Thr Gly Glu Glu Ala Glu Glu Val Gly Leu Lys Gly Glu Arg Ser Glu

65 70 75 80
 Leu Leu Leu Ser Glu Lys Val Val Asp Ala Arg Lys Ser Thr Trp His
 85 90 95
 Val Phe Pro Val Ser Ser Ser Ile Gln Arg Leu Leu Asp Gln Gly Lys
 100 105 110
 Ser Ser Leu Asp Val Arg Ile Ala Cys Glu Gln Cys Gln Glu Ser Gly
 115 120 125
 Ala Ser Leu Val Leu Leu Gly Lys Lys Lys Lys Lys Glu Glu Glu Gly
 130 135 140
 Glu Gly Lys Lys Lys Gly Gly Gly Glu Gly Gly Ala Gly Ala Asp Glu
 145 150 155 160
 Glu Lys Glu Gln Ser His Arg Pro Phe Leu Met Leu Gln Ala Arg Gln
 165 170 175
 Ser Glu Asp His Pro His Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp
 180 185 190
 Gly Lys Val Asn Ile Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys
 195 200 205
 Asp Ile Gly Trp Asn Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala
 210 215 220
 Asn Tyr Cys Glu Gly Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly
 225 230 235 240
 Ser Ser Leu Ser Phe His Ser Thr Val Ile Asn His Tyr Arg Met Arg
 245 250 255
 Gly His Ser Pro Phe Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys
 260 265 270
 Leu Arg Pro Met Ser Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile
 275 280 285
 Lys Lys Asp Ile Gln Asn Met Ile Val Glu Glu Cys Gly Cys Ser
 290 295 300

<210> 96

<211> 194

<212> PRT

<213> Homo sapiens

<400> 96

Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu
 1 5 10 15

Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro
 20 25 30

Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
 35 40 45

Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile

50 55 60
 Ser Ala Leu Arg Lys Glu Thr Cys Asn Xaa Ser Asn Met Cys Glu Lys
 65 70 75 80
 Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys
 85 90 95
 Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln
 100 105 110
 Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser
 115 120 125
 Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp
 130 135 140
 Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys
 145 150 155 160
 Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile
 165 170 175
 Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg
 180 185 190
 Gln Met

<210> 97
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 97
 Met Asn Ser Phe Ser Thr Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
 1 5 10 15
 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
 20 25 30
 Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu
 35 40 45
 Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
 50 55 60
 Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
 65 70 75 80
 Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
 85 90 95
 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu
 100 105 110
 Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His
 115 120 125
 Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala

130

135

140

Leu Arg Gln Met
145

<210> 98

<211> 220

<212> PRT

<213> Homo sapiens

<400> 98

Met Pro Arg Leu Phe Leu Phe His Leu Leu Glu Phe Cys Leu Leu Leu
1 5 10 15

Asn Gln Phe Ser Arg Ala Val Ala Ala Lys Trp Lys Asp Asp Val Ile
20 25 30

Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly
35 40 45

Met Ser Thr Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln
50 55 60

Thr Pro Arg Pro Val Ala Ala Gly Asp Phe Ile Gln Thr Val Ser Leu
65 70 75 80

Gly Ile Ser Pro Asp Gly Gly Lys Ala Leu Arg Thr Gly Ser Cys Phe
85 90 95

Thr Arg Glu Phe Leu Gly Ala Leu Ser Lys Leu Val Pro Ser Phe Ile
100 105 110

Asn Lys Asp Thr Glu Thr Ile Ile Ile Met Leu Glu Phe Ile Ala Asn
115 120 125

Leu Pro Pro Glu Leu Lys Ala Ala Leu Ser Glu Arg Gln Pro Ser Leu
130 135 140

Pro Glu Leu Gln Gln Tyr Val Pro Xaa Leu Lys Asp Ser Ser Leu Leu
145 150 155 160

Phe Glu Glu Phe Lys Lys Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala
165 170 175

Asp Ser Asn Pro Ser Glu Leu Lys Tyr Leu Gly Leu Asp Thr His Ser
180 185 190

Gln Lys Lys Arg Arg Pro Tyr Val Ala Leu Phe Glu Lys Cys Cys Leu
195 200 205

Ile Gly Cys Thr Lys Arg Ser Leu Ala Lys Tyr Cys
210 215 220

<210> 99

<211> 87

<212> PRT

<213> Homo sapiens

<400> 99

Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
 1 5 10 15
 Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
 20 25 30
 Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val
 35 40 45
 Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val
 50 55 60
 Gly Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln Glu Tyr
 65 70 75 80
 Val Tyr Asp Leu Glu Leu Asn
 85

<210> 100

<211> 731

<212> PRT

<213> Homo sapiens

<400> 100

Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys
 1 5 10 15
 Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp
 20 25 30
 Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
 35 40 45
 Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
 50 55 60
 Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp
 65 70 75 80
 Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln
 85 90 95
 Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His
 100 105 110
 Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu
 115 120 125
 Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu
 130 135 140
 Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val
 145 150 155 160
 Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn
 165 170 175
 Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala
 180 185 190

Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe
 195 200 205
 Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu
 210 215 220
 Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu
 225 230 235 240
 Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
 245 250 255
 Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
 260 265 270
 Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
 275 280 285
 Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
 290 295 300
 Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
 305 310 315 320
 Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
 325 330 335
 Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser
 340 345 350
 Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys
 355 360 365
 Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro
 370 375 380
 Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln
 385 390 395 400
 Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
 405 410 415
 Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe
 420 425 430
 Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser
 435 440 445
 Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser
 450 455 460
 Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
 465 470 475 480
 Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly
 485 490 495
 Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
 500 505 510
 Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Thr Pro Gln Phe Gly Gly

515 520 525
 Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln
 530 535 540
 Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val
 545 550 555 560
 Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro
 565 570 575
 Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys
 580 585 590
 Lys Glu Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys
 595 600 605
 Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe
 610 615 620
 Thr Gly Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn
 625 630 635 640
 Lys Gln Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp
 645 650 655
 Cys Asn Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro
 660 665 670
 Met Tyr Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile
 675 680 685
 Cys Gly Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val
 690 695 700
 Cys Val Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn
 705 710 715 720
 Leu Pro Gln Asp Pro Ala Pro Cys Pro Arg Ser
 725 730

<210> 101

<211> 555

<212> PRT

<213> Homo sapiens

<400> 101

Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys
 1 5 10 15
 Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp
 20 25 30
 Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
 35 40 45
 Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
 50 55 60
 Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp

65	70	75	80
Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln	85	90	95
Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His	100	105	110
Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu	115	120	125
Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu	130	135	140
Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val	145	150	155
Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn	165	170	175
Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala	180	185	190
Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe	195	200	205
Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu	210	215	220
Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu	225	230	235
Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr	245	250	255
Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile	260	265	270
Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg	275	280	285
Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu	290	295	300
Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His	305	310	315
Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys	325	330	335
Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser	340	345	350
Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys	355	360	365
Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro	370	375	380
Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln	385	390	395
			400

Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
 405 410 415

Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe
 420 425 430

Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser
 435 440 445

Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser
 450 455 460

Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
 465 470 475 480

Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly
 485 490 495

Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
 500 505 510

Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Thr Pro Gln Phe Gly Gly
 515 520 525

Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln
 530 535 540

Asp Cys Pro Ile Gly Glu Pro Arg Ser Pro Gly
 545 550 555

<210> 102

<211> 546

<212> PRT

<213> Homo sapiens

<400> 102

Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys
 1 5 10 15

Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp
 20 25 30

Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
 35 40 45

Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
 50 55 60

Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp
 65 70 75 80

Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln
 85 90 95

Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His
 100 105 110

Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu
 115 120 125

Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu
 130 135 140
 Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val
 145 150 155 160
 Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn
 165 170 175
 Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala
 180 185 190
 Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe
 195 200 205
 Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu
 210 215 220
 Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu
 225 230 235 240
 Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
 245 250 255
 Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
 260 265 270
 Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
 275 280 285
 Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
 290 295 300
 Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
 305 310 315 320
 Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
 325 330 335
 Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser
 340 345 350
 Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys
 355 360 365
 Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro
 370 375 380
 Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln
 385 390 395 400
 Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
 405 410 415
 Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe
 420 425 430
 Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser
 435 440 445

Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser
450 455 460

Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
465 470 475 480

Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ser Lys Cys Glu Val Arg
485 490 495

Cys Lys Gly Glu His Gly Gln Gln Leu Cys Pro Ala Gly Cys Leu Gly
500 505 510

Ile Cys Ser Leu Gln Phe Gln Trp Gly His Arg Ser Arg Lys Val Thr
515 520 525

Tyr Leu Gly Glu Thr Asn Arg Arg Gln Ser Pro Ala Gly Ser Ala Thr
530 535 540

Ser Phe
545

<210> 103
<211> 459
<212> PRT
<213> Homo sapiens

<400> 103
Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys
1 5 10 15

Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp
20 25 30

Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
35 40 45

Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
50 55 60

Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp
65 70 75 80

Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln
85 90 95

Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His
100 105 110

Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu
115 120 125

Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu
130 135 140

Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val
145 150 155 160

Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn
165 170 175

Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala
 180 185 190

Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe
 195 200 205

Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu
 210 215 220

Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu
 225 230 235 240

Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
 245 250 255

Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
 260 265 270

Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
 275 280 285

Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
 290 295 300

Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
 305 310 315 320

Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
 325 330 335

Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser
 340 345 350

Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys
 355 360 365

Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro
 370 375 380

Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln
 385 390 395 400

Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
 405 410 415

Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Cys
 420 425 430

Lys His Leu Ser Leu Ser Gly Thr Trp Arg Thr Asp Leu Ser Leu Leu
 435 440 445

Ser Ser Pro Arg Ala Ala Pro Gln His Val Tyr
 450 455

<210> 104

<211> 363

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ala	Ala	Leu	Met	Thr	Pro	Gly	Thr	Gly	Ala	Pro	Pro	Ala	Pro	Gly	1	5	10	15
Asp	Phe	Ser	Gly	Glu	Gly	Ser	Gln	Gly	Leu	Pro	Asp	Pro	Ser	Pro	Glu	20	25	30	
Pro	Lys	Gln	Leu	Pro	Glu	Leu	Ile	Arg	Met	Lys	Arg	Asp	Gly	Gly	Arg	35	40	45	
Leu	Ser	Glu	Ala	Asp	Ile	Arg	Gly	Phe	Val	Ala	Ala	Val	Val	Asn	Gly	50	55	60	
Ser	Ala	Gln	Gly	Ala	Gln	Ile	Gly	Ala	Met	Leu	Met	Ala	Ile	Arg	Leu	65	70	75	80
Arg	Gly	Met	Asp	Leu	Glu	Glu	Thr	Ser	Val	Leu	Thr	Gln	Ala	Leu	Ala	85	90	95	
Gln	Ser	Gly	Gln	Gln	Leu	Glu	Trp	Pro	Glu	Ala	Trp	Arg	Gln	Gln	Leu	100	105	110	
Val	Asp	Lys	His	Ser	Thr	Gly	Gly	Val	Gly	Asp	Lys	Val	Ser	Leu	Val	115	120	125	
Leu	Ala	Pro	Ala	Leu	Ala	Ala	Cys	Gly	Cys	Lys	Val	Pro	Met	Ile	Ser	130	135	140	
Gly	Arg	Gly	Leu	Gly	His	Thr	Gly	Gly	Thr	Leu	Asp	Lys	Leu	Glu	Ser	145	150	155	160
Ile	Pro	Gly	Phe	Asn	Val	Ile	Gln	Ser	Pro	Glu	Gln	Met	Gln	Val	Leu	165	170	175	
Leu	Asp	Gln	Ala	Gly	Cys	Cys	Ile	Val	Gly	Gln	Ser	Glu	Gln	Leu	Val	180	185	190	
Pro	Ala	Asp	Gly	Ile	Leu	Tyr	Ala	Ala	Arg	Asp	Val	Thr	Ala	Thr	Val	195	200	205	
Asp	Ser	Leu	Pro	Leu	Ile	Thr	Ala	Ser	Ile	Leu	Ser	Lys	Lys	Leu	Val	210	215	220	
Glu	Gly	Leu	Ser	Ala	Leu	Val	Val	Asp	Val	Lys	Phe	Gly	Gly	Ala	Ala	225	230	235	240
Val	Phe	Pro	Asn	Gln	Glu	Gln	Ala	Arg	Glu	Leu	Ala	Lys	Thr	Leu	Val	245	250	255	
Gly	Val	Gly	Ala	Ser	Leu	Gly	Leu	Arg	Val	Ala	Ala	Ala	Leu	Thr	Ala	260	265	270	
Met	Asp	Lys	Pro	Leu	Gly	Arg	Cys	Val	Gly	His	Ala	Leu	Glu	Val	Glu	275	280	285	
Glu	Ala	Leu	Leu	Cys	Met	Asp	Gly	Ala	Gly	Pro	Pro	Asp	Leu	Arg	Asp	290	295	300	
Leu	Val	Thr	Thr	Leu	Gly	Gly	Ala	Leu	Leu	Trp	Leu	Ser	Gly	His	Ala	305	310	315	320
Gly	Thr	Gln	Ala	Gln	Gly	Ala	Ala	Arg	Val	Ala	Ala	Ala	Arg	Ala	Leu				

325 330 335

Gln Glu Ala Leu Val Leu Ser Asp Arg Ala Pro Phe Ala Ala Pro Ser
340 345 350

Pro Phe Ala Glu Leu Val Leu Pro Pro Gln Gln
355 360

<210> 105
<211> 442
<212> PRT
<213> Homo sapiens

<400> 105

Met Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly
1 5 10 15

Asp Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu
20 25 30

Pro Lys Gln Leu Pro Glu Leu Ile Arg Met Lys Arg Asp Gly Gly Arg
35 40 45

Leu Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly
50 55 60

Ser Ala Gln Gly Ala Gln Ile Gly Ala Met Leu Met Ala Ile Arg Leu
65 70 75 80

Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln Ala Leu Ala
85 90 95

Gln Ser Gly Gln Gln Leu Glu Trp Pro Glu Ala Trp Arg Gln Gln Leu
100 105 110

Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Lys Val Ser Leu Val
115 120 125

Leu Ala Pro Ala Leu Ala Ala Cys Gly Cys Lys Val Pro Met Ile Ser
130 135 140

Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu Ser
145 150 155 160

Ile Pro Gly Phe Asn Val Ile Gln Ser Pro Glu Gln Met Gln Val Leu
165 170 175

Leu Asp Gln Ala Gly Cys Cys Ile Val Gly Gln Ser Glu Gln Leu Val
180 185 190

Pro Ala Asp Gly Ile Leu Tyr Ala Ala Arg Asp Val Thr Ala Thr Val
195 200 205

Asp Ser Leu Pro Leu Ile Thr Gly Trp Arg Gly Ser Gln Pro Arg Ala
210 215 220

Arg Val Ala Ala Ala Leu Thr Ala Met Asp Lys Pro Leu Gly Arg Cys
225 230 235 240

Val Gly His Ala Leu Glu Val Glu Glu Ala Leu Leu Cys Met Asp Gly

245 250 255

Ala Gly Pro Pro Asp Leu Arg Asp Leu Val Thr Thr Leu Gly Gly Ala
260 265 270

Leu Leu Trp Leu Ser Gly His Ala Gly Thr Gln Ala Gln Gly Ala Ala
275 280 285

Arg Val Ala Ala Ala Leu Asp Asp Gly Ser Ala Leu Gly Arg Phe Glu
290 295 300

Arg Met Leu Ala Ala Gln Gly Val Asp Pro Gly Leu Ala Arg Ala Leu
305 310 315 320

Cys Ser Gly Ser Pro Ala Glu Arg Arg Gln Leu Leu Pro Arg Ala Arg
325 330 335

Glu Gln Glu Glu Leu Leu Ala Pro Ala Asp Gly Thr Val Glu Leu Val
340 345 350

Arg Ala Leu Pro Leu Ala Leu Val Leu His Glu Leu Gly Ala Gly Arg
355 360 365

Ser Arg Ala Gly Glu Pro Leu Arg Leu Gly Val Gly Ala Glu Leu Leu
370 375 380

Val Asp Val Gly Gln Arg Leu Arg Arg Gly Thr Pro Trp Leu Arg Val
385 390 395 400

His Arg Asp Gly Pro Ala Leu Ser Gly Pro Gln Ser Arg Ala Leu Gln
405 410 415

Glu Ala Leu Val Leu Ser Asp Arg Ala Pro Phe Ala Ala Pro Ser Pro
420 425 430

Phe Ala Glu Leu Val Leu Pro Pro Gln Gln
435 440

<210> 106
<211> 323
<212> PRT
<213> Homo sapiens

<400> 106

Met Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly
1 5 10 15

Asp Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu
20 25 30

Pro Lys Gln Leu Pro Glu Leu Ile Arg Met Lys Arg Asp Gly Gly Arg
35 40 45

Leu Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly
50 55 60

Ser Ala Gln Gly Ala Gln Ile Gly Ala Met Leu Met Ala Ile Arg Leu
65 70 75 80

Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln Ala Leu Ala

85										90					95				
Gln	Ser	Gly	Gln	Gln	Leu	Glu	Trp	Pro	Glu	Ala	Trp	Arg	Gln	Gln	Leu				
			100					105					110						
Val	Asp	Lys	His	Ser	Thr	Gly	Gly	Val	Gly	Asp	Lys	Val	Ser	Leu	Val				
		115					120					125							
Leu	Ala	Pro	Ala	Leu	Ala	Ala	Cys	Gly	Cys	Lys	Val	Pro	Met	Ile	Ser				
	130					135					140								
Gly	Arg	Gly	Leu	Gly	His	Thr	Gly	Gly	Thr	Leu	Asp	Lys	Leu	Glu	Ser				
145					150					155					160				
Ile	Pro	Gly	Phe	Asn	Val	Ile	Gln	Ser	Pro	Glu	Gln	Met	Gln	Val	Leu				
				165					170					175					
Leu	Asp	Gln	Ala	Gly	Cys	Cys	Ile	Val	Gly	Gln	Ser	Glu	Gln	Leu	Val				
			180						185					190					
Pro	Ala	Asp	Gly	Ile	Leu	Tyr	Ala	Ala	Arg	Asp	Val	Thr	Ala	Thr	Val				
		195					200					205							
Asp	Ser	Leu	Pro	Leu	Ile	Thr	Gly	Trp	Arg	Gly	Ser	Gln	Pro	Arg	Ala				
	210					215					220								
Arg	Val	Ala	Ala	Ala	Leu	Thr	Ala	Met	Asp	Lys	Pro	Leu	Gly	Arg	Cys				
225					230					235					240				
Val	Gly	His	Ala	Leu	Glu	Val	Glu	Glu	Ala	Leu	Leu	Cys	Met	Asp	Gly				
				245					250					255					
Ala	Gly	Pro	Pro	Asp	Leu	Arg	Asp	Leu	Val	Thr	Thr	Leu	Gly	Gly	Ala				
			260					265						270					
Leu	Leu	Trp	Leu	Ser	Gly	His	Ala	Gly	Thr	Gln	Ala	Gln	Gly	Ala	Ala				
		275					280						285						
Arg	Val	Ala	Ala	Ala	Arg	Ala	Leu	Gln	Glu	Ala	Leu	Val	Leu	Ser	Asp				
	290					295					300								
Arg	Ala	Pro	Phe	Ala	Ala	Pro	Ser	Pro	Phe	Ala	Glu	Leu	Val	Leu	Pro				
305					310					315					320				
Pro Gln Gln																			

<210> 107

<211> 481

<212> PRT

<213> Homo sapiens

<400> 107

Met	Ala	Ser	Arg	Leu	Thr	Leu	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Ala
1				5					10					15

Gly	Asp	Arg	Ala	Ser	Ser	Asn	Pro	Asn	Ala	Thr	Ser	Ser	Val	Ile	Ser
			20					25					30		

Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser Leu Pro Thr

35					40					45						
Thr	Asn	Ser	Thr	Thr	Asn	Ser	Ala	Thr	Lys	Ile	Thr	Ala	Asn	Thr	Thr	
50					55					60						
Asp	Glu	Pro	Thr	Thr	Gln	Pro	Thr	Thr	Glu	Pro	Thr	Thr	Gln	Pro	Thr	
65					70					75					80	
Ile	Gln	Pro	Thr	Gln	Pro	Thr	Thr	Gln	Leu	Pro	Thr	Asp	Ser	Pro	Thr	
85					90					95						
Gln	Pro	Thr	Thr	Gly	Ser	Phe	Cys	Pro	Gly	Pro	Val	Thr	Leu	Cys	Ser	
100					105					110						
Asp	Leu	Glu	Ser	His	Ser	Thr	Glu	Ala	Val	Leu	Gly	Asp	Ala	Leu	Val	
115					120					125						
Asp	Phe	Ser	Leu	Lys	Leu	Tyr	His	Ala	Phe	Ser	Ala	Met	Lys	Lys	Val	
130					135					140						
Glu	Thr	Asn	Met	Ala	Phe	Ser	Pro	Phe	Ser	Ile	Ala	Ser	Leu	Leu	Thr	
145					150					155					160	
Gln	Val	Leu	Leu	Gly	Ala	Gly	Glu	Asn	Thr	Lys	Thr	Asn	Leu	Glu	Ser	
165					170					175						
Ile	Leu	Ser	Tyr	Pro	Lys	Asp	Phe	Thr	Cys	Val	His	Gln	Ala	Leu	Lys	
180					185					190						
Gly	Phe	Thr	Thr	Lys	Gly	Val	Thr	Ser	Val	Ser	Gln	Ile	Phe	His	Ser	
195					200					205						
Pro	Asp	Leu	Ala	Ile	Arg	Asp	Thr	Phe	Val	Asn	Ala	Ser	Arg	Thr	Leu	
210					215					220						
Tyr	Ser	Ser	Ser	Pro	Arg	Val	Leu	Ser	Asn	Asn	Ser	Asp	Ala	Asn	Leu	
225					230					235					240	
Glu	Leu	Ile	Asn	Thr	Trp	Val	Ala	Lys	Asn	Thr	Asn	Asn	Lys	Ile	Ser	
245					250					255						
Arg	Leu	Leu	Asp	Ser	Leu	Pro	Ser	Asp	Thr	Arg	Leu	Val	Leu	Leu	Asn	
260					265					270						
Ala	Ile	Tyr	Leu	Ser	Ala	Lys	Trp	Lys	Thr	Thr	Phe	Asp	Pro	Lys	Lys	
275					280					285						
Thr	Arg	Met	Glu	Pro	Phe	His	Phe	Lys	Asn	Ser	Val	Ile	Lys	Val	Pro	
290					295					300						
Met	Met	Asn	Ser	Lys	Lys	Tyr	Pro	Val	Ala	His	Phe	Ile	Asp	Gln	Thr	
305					310					315					320	
Leu	Lys	Ala	Lys	Val	Gly	Gln	Leu	Gln	Leu	Ser	His	Asn	Leu	Ser	Leu	
325					330					335						
Val	Ile	Leu	Val	Pro	Gln	Asn	Leu	Lys	His	Arg	Leu	Glu	Asp	Met	Glu	
340					345					350						
Gln	Ala	Leu	Ser	Pro	Ser	Val	Phe	Lys	Ala	Ile	Met	Glu	Lys	Leu	Glu	
355					360					365						

Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg Ile Lys Val
 370 375 380

Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu Glu Phe Phe
 385 390 395 400

Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu Asp Pro Asp
 405 410 415

Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu Leu Thr Glu
 420 425 430

Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val Ala Arg Thr
 435 440 445

Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val Leu Trp Asp
 450 455 460

Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr Asp Pro Arg
 465 470 475 480

Ala

<210> 108
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Met Asp Glu Glu Glu Val Glu Val Ser Leu Pro Arg Phe Lys Leu
 1 5 10 15

Glu Glu Ser Tyr Asp Met Glu Ser Val Leu Arg Asn Leu Gly Met Thr
 20 25 30

Asp Ala Phe Glu Leu Gly Lys Ala Asp Phe Ser Gly Met Ser Gln Thr
 35 40 45

Asp Leu Ser Leu Ser Lys Val Val His Lys Ser Phe Val Glu Val Asn
 50 55 60

Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Ala Ala Ile Met Met Met
 65 70 75 80

Arg Cys Ala Arg Phe Val Pro Arg Phe Cys Ala Asp His Pro Phe Leu
 85 90 95

Phe Phe Ile Gln His Ser Lys Thr Asn Gly Ile Leu Phe Cys Gly Arg
 100 105 110

Phe Ser Ser Pro
 115

<210> 109
 <211> 319
 <212> PRT
 <213> Homo sapiens

<400> 109

Met Asp Val Leu Ala Glu Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu
 1 5 10 15

Lys Thr Leu Gly Lys Asp Asn Ser Lys Asn Val Phe Phe Ser Pro Met
 20 25 30

Ser Met Ser Cys Ala Leu Ala Met Val Tyr Met Gly Ala Lys Gly Asn
 35 40 45

Thr Ala Ala Gln Met Ala Gln Ile Leu Ser Phe Asn Lys Ser Gly Gly
 50 55 60

Gly Gly Asp Ile His Gln Gly Phe Gln Ser Leu Leu Thr Glu Val Asn
 65 70 75 80

Lys Thr Gly Thr Gln Tyr Leu Leu Arg Val Ala Asn Arg Leu Phe Gly
 85 90 95

Glu Lys Ser Cys Asp Phe Leu Ser Ser Phe Arg Asp Ser Cys Gln Lys
 100 105 110

Phe Tyr Gln Ala Glu Met Glu Glu Leu Asp Phe Ile Ser Ala Val Glu
 115 120 125

Lys Ser Arg Lys His Ile Asn Thr Trp Val Ala Glu Lys Thr Glu Gly
 130 135 140

Lys Ile Ala Glu Leu Leu Ser Pro Gly Ser Val Asp Pro Leu Thr Arg
 145 150 155 160

Leu Val Leu Val Asn Ala Val Tyr Phe Arg Gly Asn Trp Asp Glu Gln
 165 170 175

Phe Asp Lys Glu Asn Thr Glu Glu Arg Leu Phe Lys Val Ser Lys Asn
 180 185 190

Glu Glu Lys Pro Val Gln Met Met Phe Lys Gln Ser Thr Phe Lys Lys
 195 200 205

Thr Tyr Ile Gly Glu Ile Phe Thr Gln Ile Leu Val Leu Pro Tyr Val
 210 215 220

Gly Lys Glu Leu Asn Met Ile Ile Met Leu Pro Asp Glu Thr Thr Asp
 225 230 235 240

Leu Arg Thr Val Glu Lys Glu Leu Thr Tyr Glu Lys Phe Val Glu Trp
 245 250 255

Thr Arg Leu Asp Met Met Asp Glu Glu Glu Val Glu Glu Gly Thr Glu
 260 265 270

Ala Ala Ala Ala Thr Ala Ala Ile Met Met Met Arg Cys Ala Arg Phe
 275 280 285

Val Pro Arg Phe Cys Ala Asp His Pro Phe Leu Phe Phe Ile Gln His
 290 295 300

Ser Lys Thr Asn Gly Ile Leu Phe Cys Gly Arg Phe Ser Ser Pro
 305 310 315

<210> 110
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 110
 Met Asp Val Leu Ala Glu Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu
 1 5 10 15
 Lys Thr Leu Gly Lys Asp Asn Ser Lys Asn Val Phe Phe Ser Pro Met
 20 25 30
 Ser Met Ser Cys Ala Leu Ala Met Val Tyr Met Gly Ala Lys Gly Asn
 35 40 45
 Thr Ala Ala Gln Met Ala Gln Ile Leu Ser Phe Asn Lys Ser Gly Gly
 50 55 60
 Gly Gly Asp Ile His Gln Gly Phe Gln Ser Leu Leu Thr Glu Val Asn
 65 70 75 80
 Lys Thr Gly Thr Gln Tyr Leu Leu Arg Glu Ser Tyr Asp Met Glu Ser
 85 90 95
 Val Leu Arg Asn Leu Gly Met Thr Asp Ala Phe Glu Leu Gly Lys Ala
 100 105 110
 Asp Phe Ser Gly Met Ser Gln Thr Asp Leu Ser Leu Ser Lys Val Val
 115 120 125
 His Lys Ser Phe Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala
 130 135 140
 Ala Thr Ala Ala Ile Met Met Met Arg Cys Ala Arg Phe Val Pro Arg
 145 150 155 160
 Phe Cys Ala Asp His Pro Phe Leu Phe Phe Ile Gln His Ser Lys Thr
 165 170 175
 Asn Gly Ile Leu Phe Cys Gly Arg Phe Ser Ser Pro
 180 185

<210> 111
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 111
 Met Asp Val Leu Ala Glu Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu
 1 5 10 15
 Lys Thr Leu Gly Lys Asp Asn Ser Lys Asn Val Phe Phe Ser Pro Met
 20 25 30
 Ser Met Ser Cys Ala Leu Ala Met Val Tyr Met Gly Ala Lys Gly Asn
 35 40 45
 Thr Ala Ala Gln Met Ala Gln Arg Phe Gln Lys Val

50

55

60

<210> 112

<211> 306

<212> PRT

<213> Homo sapiens

<400> 112

Met His Lys Thr Ala Ser Gln Arg Leu Phe Pro Gly Pro Ser Tyr Gln
 1 5 10 15

Asn Ile Lys Ser Ile Met Glu Asp Ser Thr Ile Leu Ser Asp Trp Thr
 20 25 30

Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr
 35 40 45

Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu
 50 55 60

Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys
 65 70 75 80

Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Leu Gly
 85 90 95

Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser Cys Ser Phe
 100 105 110

Ile Gln Asn Leu Val Ser Ala Ser Leu Gly Ser Thr Ser Lys Asn Thr
 115 120 125

Ser Pro Met Arg Asn Ser Phe Ala His Ser Leu Ser Pro Thr Leu Glu
 130 135 140

His Ser Ser Leu Phe Ser Gly Ser Tyr Ser Ser Leu Ser Pro Asn Pro
 145 150 155 160

Leu Asn Ser Arg Ala Val Glu Asp Ile Ser Ser Ser Arg Thr Asn Pro
 165 170 175

Tyr Ser Tyr Ala Met Ser Thr Glu Glu Ala Arg Phe Leu Thr Tyr His
 180 185 190

Met Trp Pro Leu Thr Phe Leu Ser Pro Ser Glu Leu Ala Arg Ala Gly
 195 200 205

Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys Gly
 210 215 220

Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met Ser Glu His
 225 230 235 240

Leu Arg His Phe Pro Asn Cys Pro Phe Leu Glu Asn Ser Leu Glu Thr
 245 250 255

Leu Arg Phe Ser Ile Ser Asn Leu Ser Met Gln Thr His Ala Ala Arg
 260 265 270

Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro Val Gln Pro Glu

275 280 285
 Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Lys Lys Leu Asn Leu
 290 295 300

 Leu Ile
 305

 <210> 113
 <211> 359
 <212> PRT
 <213> Homo sapiens

 <400> 113
 Met His Ser Ser Met Lys Thr Ser Leu Phe Phe His Ile Val Met Gln
 1 5 10 15

 Leu Gly Phe Ser Ala Leu Ser Phe Phe Tyr Pro Phe Phe Asn Ser Ser
 20 25 30

 Tyr Tyr Val Gln Met Ile Ile Leu Ser Arg Phe Gly Cys Pro Asp Gln
 35 40 45

 Asn Gly Asp Arg Val Glu Arg Cys Asp Ser Lys Ala Leu Asp Arg Val
 50 55 60

 Ile Xaa Leu Pro Phe Ser Pro Pro Pro Arg Ser Pro Pro Asp Arg Gly
 65 70 75 80

 Glu His Met Ser Ala Pro Ala Ala Lys Val Ser Lys Lys Glu Leu Asn
 85 90 95

 Ser Asn His Asp Gly Ala Asp Glu Thr Ser Glu Lys Glu Gln Gln Glu
 100 105 110

 Ala Ile Glu His Ile Asp Glu Val Gln Asn Glu Ile Asp Arg Leu Asn
 115 120 125

 Glu Gln Ala Ser Glu Glu Ile Leu Lys Val Glu Gln Lys Tyr Asn Lys
 130 135 140

 Leu Arg Gln Pro Phe Phe Gln Lys Arg Ser Glu Leu Ile Ala Lys Ile
 145 150 155 160

 Pro Asn Phe Trp Val Thr Thr Phe Val Asn His Pro Gln Val Ser Ala
 165 170 175

 Leu Leu Gly Glu Glu Asp Glu Glu Ala Leu His Tyr Leu Thr Arg Val
 180 185 190

 Glu Val Thr Glu Phe Glu Asp Ile Lys Ser Gly Tyr Arg Ile Asp Phe
 195 200 205

 Tyr Phe Asp Glu Asn Pro Tyr Phe Glu Asn Lys Val Leu Ser Lys Glu
 210 215 220

 Phe His Leu Asn Glu Ser Gly Asp Pro Ser Ser Lys Ser Thr Glu Ile
 225 230 235 240

 Lys Trp Lys Ser Gly Lys Asp Leu Thr Lys Arg Ser Ser Gln Thr Gln

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<210> 114
<211> 261
<212> PRT
<213> Homo sapiens
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<400> 114
Met Ser Ala Pro Ala Ala Lys Val Ser Lys Lys Glu Leu Asn Ser Asn
  1             5             10             15
His Asp Gly Ala Asp Glu Thr Ser Glu Lys Glu Gln Gln Glu Ala Ile
             20             25             30
Glu His Ile Asp Glu Val Gln Asn Glu Ile Asp Arg Leu Asn Glu Gln
             35             40             45
Ala Ser Glu Glu Ile Leu Lys Val Glu Gln Lys Tyr Asn Lys Leu Arg
             50             55             60
Gln Pro Phe Phe Gln Lys Arg Ser Glu Leu Ile Ala Lys Ile Pro Asn
             65             70             75             80
Phe Trp Val Thr Thr Phe Val Asn His Pro Gln Val Ser Ala Leu Leu
             85             90             95
Gly Glu Glu Asp Glu Glu Ala Leu His Tyr Leu Thr Arg Val Glu Val
             100             105             110
Thr Glu Phe Glu Asp Ile Lys Ser Gly Tyr Arg Ile Asp Phe Tyr Phe
             115             120             125
Asp Glu Asn Pro Tyr Phe Glu Asn Lys Val Leu Ser Lys Glu Phe His
             130             135             140
Leu Asn Glu Ser Gly Asp Pro Ser Ser Lys Ser Thr Glu Ile Lys Trp
             145             150             155             160
Lys Ser Gly Lys Asp Leu Thr Lys Arg Ser Ser Gln Thr Gln Asn Lys

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				165				170				175				
Ala	Ser	Arg	Lys	Arg	Gln	His	Glu	Glu	Pro	Glu	Ser	Phe	Phe	Thr	Trp	
180								185				190				
Phe	Thr	Asp	His	Ser	Asp	Ala	Gly	Ala	Asp	Glu	Leu	Gly	Glu	Val	Ile	
195								200				205				
Lys	Asp	Asp	Ile	Trp	Pro	Asn	Pro	Leu	Gln	Tyr	Tyr	Leu	Val	Pro	Asp	
210												220				
Met	Asp	Asp	Glu	Glu	Gly	Glu	Gly	Glu	Glu	Asp	Asp	Asp	Asp	Asp	Glu	
225					230				235				240			
Glu	Glu	Glu	Gly	Leu	Glu	Asp	Ile	Asp	Glu	Glu	Gly	Asp	Gly	Gly	Gly	
				245				250				255				
Gly	Gly	Lys	Gly	Pro												
260																

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<210> 115
<211> 260
<212> PRT
<213> Homo sapiens
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<400> 115																
Met	Leu	Ile	Ala	Ala	Gly	Pro	Ala	Arg	Thr	Gly	Val	Gly	Pro	Ala	Arg	
1				5					10					15		
Ile	Lys	Gly	Ala	Gln	Ala	Gly	Trp	Ala	Phe	His	Arg	Pro	Ser	Ala	Leu	
			20					25					30			
Cys	Ser	Arg	Gly	Ala	Gly	Gln	Ala	Xaa	Ala	Ser	Glu	Leu	Ala	Ser	Arg	
		35					40					45				
His	Arg	Gly	Gly	Ala	Ala	Ala	Val	Arg	Thr	Arg	Gln	Ala	Asn	Pro	Thr	
	50					55					60					
Gln	Lys	Ser	Pro	Pro	Pro	Asp	Ser	Gln	Val	Ala	Ala	Ala	Ser	Leu	Ala	
65					70					75					80	
His	Ala	Glu	Ser	Gly	Gly	Ala	Gly	Ser	Pro	Leu	Arg	Pro	Ala	Ser	Ala	
				85					90					95		
Leu	Ser	Ser	Ser	Pro	Phe	Pro	Phe	Phe	Ser	Leu	Ser	Ser	Pro	Leu	Ser	
			100					105					110			
Leu	Pro	Ala	Phe	Ala	Gln	Pro	Arg	Ala	Met	Ser	Asp	Ala	Ser	Leu	Arg	
		115					120					125				
Ser	Thr	Ser	Thr	Met	Glu	Arg	Leu	Val	Ala	Arg	Gly	Thr	Phe	Pro	Val	
	130					135					140					
Leu	Val	Arg	Thr	Ser	Ala	Cys	Arg	Ser	Leu	Phe	Gly	Pro	Val	Asp	His	
145					150					155					160	
Glu	Glu	Leu	Ser	Arg	Glu	Leu	Gln	Ala	Arg	Leu	Ala	Glu	Leu	Asn	Ala	
				165				170						175		
Glu	Asp	Gln	Asn	Arg	Trp	Asp	Tyr	Asp	Phe	Gln	Gln	Asp	Met	Pro	Leu	

180 185 190
 Arg Gly Pro Gly Arg Leu Gln Trp Thr Glu Val Asp Ser Asp Ser Val
 195 200 205
 Pro Ala Phe Tyr Arg Glu Thr Val Gln Ile Phe Phe Ala Lys Arg Lys
 210 215 220
 Arg Ser Ala Pro Glu Lys Ser Ser Gly Asp Val Pro Ala Pro Cys Pro
 225 230 235 240
 Ser Pro Ser Ala Ala Pro Gly Val Gly Ser Val Glu Gln Thr Pro Arg
 245 250 255
 Lys Arg Leu Arg
 260

<210> 116
 <211> 582
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Met Thr Leu Arg His Leu Pro Phe Ile Leu Leu Leu Ile Leu Ser
 1 5 10 15
 Gly Glu Leu Tyr Ala Glu Glu Lys Gln Cys Asp Phe Pro Thr Val Glu
 20 25 30
 Asn Gly Arg Ile Ala Gln Tyr Tyr Tyr Thr Phe Lys Ser Phe Tyr Phe
 35 40 45
 Pro Met Ser Val Asp Lys Lys Leu Ser Phe Phe Cys Leu Ala Gly Tyr
 50 55 60
 Ala Thr Glu Ser Gly Lys Gln Glu Glu Gln Ile Arg Cys Thr Ala Glu
 65 70 75 80
 Gly Trp Ser Pro Asn Pro Arg Cys Tyr Lys Lys Cys Leu Lys Pro Asp
 85 90 95
 Leu Arg Asn Gly Tyr Val Ser Asn Asp Lys Val Leu Tyr Lys Leu Gln
 100 105 110
 Glu Arg Met Ser Tyr Gly Cys Ser Ser Gly Tyr Lys Thr Thr Gly Gly
 115 120 125
 Lys Asp Glu Glu Val Val His Cys Leu Ser Ala Gly Trp Ser Ser Gln
 130 135 140
 Pro Ser Cys Arg Lys Glu Gln Glu Thr Cys Leu Ala Pro Glu Leu Glu
 145 150 155 160
 His Gly Asn Tyr Ser Thr Thr Gln Arg Thr Phe Lys Val Lys Asp Ile
 165 170 175
 Val Ala Tyr Thr Cys Thr Ala Gly Tyr Tyr Thr Thr Thr Gly Lys Gln
 180 185 190
 Thr Gly Glu Ala Glu Cys Gln Ala Asn Gly Trp Ser Leu Thr Pro Gln

195					200					205					
Cys	Asn	Lys	Leu	Met	Cys	Ser	Ser	Leu	Arg	Leu	Ile	Glu	Asn	Gly	Tyr
210					215					220					
Phe	His	Pro	Val	Lys	Gln	Thr	Tyr	Glu	Glu	Gly	Asp	Val	Val	Gln	Phe
225					230					235					240
Phe	Cys	His	Glu	Asn	Tyr	Tyr	Leu	Ser	Gly	Ser	Asp	Leu	Ile	Gln	Cys
				245					250					255	
Tyr	Asn	Phe	Gly	Trp	Tyr	Pro	Glu	Ser	Pro	Ile	Cys	Glu	Gly	Arg	Arg
			260					265					270		
Asn	Arg	Cys	Pro	Pro	Pro	Pro	Val	Pro	Leu	Asn	Ser	Lys	Ile	Gln	Pro
		275					280					285			
His	Ser	Thr	Thr	Tyr	Arg	His	Gly	Glu	Arg	Val	His	Ile	Glu	Cys	Glu
	290					295					300				
Leu	Asn	Phe	Val	Ile	Gln	Gly	Ser	Glu	Glu	Leu	Leu	Cys	Glu	Asn	Gly
305					310					315					320
Lys	Trp	Thr	Glu	Pro	Pro	Lys	Cys	Ile	Glu	Glu	Lys	Glu	Lys	Val	Ala
				325					330					335	
Cys	Glu	Gln	Pro	Pro	Ser	Val	Glu	Asn	Gly	Val	Ala	His	Pro	His	Ser
			340					345					350		
Glu	Ile	Tyr	Tyr	Ser	Gly	Asp	Lys	Val	Thr	Tyr	Arg	Cys	Gly	Gly	Gly
	355						360					365			
Tyr	Ser	Leu	Arg	Gly	Ser	Ser	Thr	Ile	Thr	Cys	Asn	Arg	Gly	Arg	Trp
	370					375					380				
Thr	Leu	Pro	Pro	Glu	Cys	Val	Glu	Asn	Ile	Glu	Asn	Cys	Lys	Pro	Pro
385					390					395					400
Pro	Asp	Ile	Ala	Asn	Gly	Val	Val	Val	Asp	Gly	Leu	Leu	Ala	Ser	Tyr
				405					410					415	
Thr	Thr	Gly	Ser	Ser	Val	Glu	Tyr	Arg	Cys	Asn	Glu	Tyr	Tyr	Leu	Leu
			420					425					430		
Lys	Gly	Ser	Glu	Thr	Ser	Arg	Cys	Glu	Gln	Gly	Ala	Trp	Ser	Ser	Pro
		435					440					445			
Pro	Val	Cys	Leu	Glu	Pro	Cys	Thr	Ile	Asp	Val	Asp	His	Met	Asn	Arg
	450					455					460				
Asn	Asn	Ile	Gln	Leu	Lys	Trp	Lys	Tyr	Glu	Gly	Lys	Ile	Leu	His	Gly
465					470					475					480
Asp	Leu	Ile	Asp	Phe	Val	Cys	Lys	Gln	Gly	Tyr	Asn	Leu	Ser	Pro	Ser
				485					490					495	
Ile	Pro	Leu	Ser	Glu	Ile	Ser	Ala	Gln	Cys	Asn	Arg	Gly	Asp	Val	Arg
			500					505					510		
Tyr	Pro	Met	Cys	Ile	Arg	Lys	Glu	Ser	Lys	Gly	Met	Cys	Ala	Ser	Pro
		515					520					525			

Pro Val Ile Arg Asn Gly Asp Ile Val Ser Ser Ala Ala Arg Thr Tyr
530 535 540

Glu Asn Gly Ser Ser Val Glu Tyr Arg Cys Phe Asp Asn His Phe Leu
545 550 555 560

Gln Gly Ser Gln Asn Val Tyr Cys Val Asp Gly Val Trp Thr Thr Pro
565 570 575

Pro Ser Cys Leu Glu Pro
580

<210> 117

<211> 576

<212> PRT

<213> Homo sapiens

<400> 117

Met Pro Trp Gly Arg Arg Pro Thr Trp Leu Leu Leu Ala Phe Leu Leu
1 5 10 15

Val Phe Leu Lys Ile Ser Ile Leu Ser Val Thr Ala Trp Gln Thr Gly
20 25 30

Asn Cys Gln Pro Gly Pro Leu Glu Arg Ser Glu Arg Ser Gly Thr Cys
35 40 45

Ala Gly Pro Ala Pro Phe Leu Val Phe Ser Gln Gly Lys Ser Ile Ser
50 55 60

Arg Ile Trp Ala Ile Pro Ser Val Ile Arg Val Asn Lys Arg Thr Gly
65 70 75 80

Gln Asn Arg Val Arg Leu Gln Gly Ser Met Leu Lys Pro Ser Ser Leu
85 90 95

Val Val Val His Pro Leu Ala Lys Pro Gly Ala Asp Pro Cys Leu Tyr
100 105 110

Arg Asn Gly Gly Cys Glu His Ile Cys Gln Glu Ser Leu Gly Thr Ala
115 120 125

Arg Cys Leu Cys Arg Glu Gly Phe Val Lys Ala Trp Asp Gly Lys Met
130 135 140

Cys Leu Pro Gln Asp Tyr Pro Ile Leu Ser Gly Glu Asn Ala Asp Leu
145 150 155 160

Ser Lys Glu Val Thr Ser Leu Ser Asn Ser Thr Gln Ala Glu Val Pro
165 170 175

Asp Asp Asp Gly Thr Glu Ser Ser Thr Leu Val Ala Glu Ile Met Val
180 185 190

Ser Gly Met Asn Tyr Glu Asp Asp Cys Gly Pro Gly Gly Cys Gly Ser
195 200 205

His Ala Arg Cys Val Ser Asp Gly Glu Thr Ala Glu Cys Gln Cys Leu
210 215 220

Lys Gly Phe Ala Arg Asp Gly Asn Leu Cys Ser Asp Ile Asp Glu Cys
 225 230 235 240
 Val Leu Ala Arg Ser Asp Cys Pro Ser Thr Ser Ser Arg Cys Ile Asn
 245 250 255
 Thr Glu Gly Gly Tyr Val Cys Arg Cys Ser Glu Gly Tyr Glu Gly Asp
 260 265 270
 Gly Ile Ser Cys Phe Asp Ile Asp Glu Cys Gln Arg Gly Ala His Asn
 275 280 285
 Cys Ala Glu Asn Ala Ala Cys Thr Asn Thr Glu Gly Gly Tyr Asn Cys
 290 295 300
 Thr Cys Ala Gly Arg Pro Ser Ser Pro Gly Leu Ser Cys Pro Asp Ser
 305 310 315 320
 Thr Ala Pro Ser Leu Leu Gly Glu Asp Gly His His Leu Asp Arg Asn
 325 330 335
 Ser Tyr Pro Gly Cys Pro Ser Ser Tyr Asp Gly Tyr Cys Leu Asn Gly
 340 345 350
 Gly Val Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys Asn Cys
 355 360 365
 Val Ile Gly Tyr Ser Gly Asp Arg Cys Gln Thr Arg Asp Leu Arg Trp
 370 375 380
 Trp Glu Leu Arg His Ala Gly Tyr Gly Gln Lys His Asp Ile Met Val
 385 390 395 400
 Val Ala Val Cys Met Val Ala Leu Val Leu Leu Leu Leu Gly Met
 405 410 415
 Trp Gly Thr Tyr Tyr Tyr Arg Thr Arg Lys Gln Leu Ser Asn Pro Pro
 420 425 430
 Lys Asn Pro Cys Asp Glu Pro Ser Gly Ser Val Ser Ser Ser Gly Pro
 435 440 445
 Asp Ser Ser Ser Gly Ala Ala Val Ala Ser Cys Pro Gln Pro Trp Phe
 450 455 460
 Val Val Leu Glu Lys His Gln Asp Pro Lys Asn Gly Ser Leu Pro Ala
 465 470 475 480
 Asp Gly Thr Asn Gly Ala Val Val Asp Ala Gly Leu Ser Pro Ser Leu
 485 490 495
 Gln Leu Gly Ser Val His Leu Thr Ser Trp Arg Gln Lys Pro His Ile
 500 505 510
 Asp Gly Met Gly Thr Gly Gln Ser Cys Trp Ile Pro Pro Ser Ser Asp
 515 520 525
 Arg Gly Pro Gln Glu Ile Glu Gly Asn Ser His Leu Pro Ser Tyr Arg
 530 535 540

Pro Val Gly Pro Glu Lys Leu His Ser Leu Gln Ser Ala Asn Gly Ser
545 550 555 560

Cys His Glu Arg Ala Pro Asp Leu Pro Arg Gln Thr Glu Pro Val Gln
565 570 575

<210> 118

<211> 550

<212> PRT

<213> Homo sapiens

<400> 118

Met Pro Trp Gly Arg Arg Pro Thr Trp Leu Leu Leu Ala Phe Leu Leu
1 5 10 15

Val Phe Leu Lys Ile Ser Ile Leu Ser Val Thr Ala Trp Gln Thr Gly
20 25 30

Asn Cys Gln Pro Gly Pro Leu Glu Arg Ser Glu Arg Ser Gly Thr Cys
35 40 45

Ala Gly Pro Ala Pro Phe Leu Val Phe Ser Gln Gly Lys Ser Ile Ser
50 55 60

Arg Ile Asp Pro Asp Gly Thr Asn His Gln Gln Leu Val Val Asp Ala
65 70 75 80

Gly Ile Ser Ala Asp Met Asp Ile His Tyr Lys Lys Glu Arg Leu Tyr
85 90 95

Trp Val Asp Val Glu Arg Gln Val Leu Leu Arg Val Phe Leu Asn Gly
100 105 110

Thr Gly Leu Glu Lys Val Cys Asn Val Glu Arg Lys Val Ser Gly Leu
115 120 125

Ala Ile Asp Trp Ile Asp Asp Glu Val Leu Trp Val Asp Gln Gln Asn
130 135 140

Gly Val Ile Thr Val Thr Asp Met Thr Gly Lys Asn Ser Arg Val Leu
145 150 155 160

Leu Ser Ser Leu Lys His Pro Ser Asn Ile Ala Val Asp Pro Ile Glu
165 170 175

Arg Leu Met Phe Trp Ser Ser Glu Val Thr Gly Ser Leu His Arg Ala
180 185 190

His Leu Lys Gly Val Asp Val Lys Thr Leu Leu Glu Thr Gly Gly Ile
195 200 205

Ser Val Leu Thr Leu Asp Val Leu Asp Lys Arg Leu Phe Trp Val Gln
210 215 220

Asp Ser Gly Glu Gly Ser His Ala Tyr Ile His Ser Cys Asp Tyr Glu
225 230 235 240

Gly Gly Ser Val Arg Leu Ile Arg His Gln Ala Arg His Ser Leu Ser
 245 250 255
 Ser Met Ala Phe Phe Gly Asp Arg Ile Phe Tyr Ser Val Leu Lys Ser
 260 265 270
 Lys Ala Ile Trp Ile Ala Asn Lys His Thr Gly Lys Asp Thr Val Arg
 275 280 285
 Ile Asn Leu His Pro Ser Phe Val Thr Pro Gly Lys Leu Met Val Val
 290 295 300
 His Pro Arg Ala Gln Pro Arg Thr Glu Asp Ala Ala Lys Asp Pro Asp
 305 310 315 320
 Pro Glu Leu Leu Lys Gln Arg Gly Arg Pro Cys Arg Phe Gly Leu Cys
 325 330 335
 Glu Arg Asp Pro Lys Ser His Ser Ser Ala Cys Ala Glu Gly Tyr Thr
 340 345 350
 Leu Ser Arg Asp Arg Lys Tyr Cys Glu Asp Val Asn Glu Cys Ala Thr
 355 360 365
 Gln Asn His Gly Cys Thr Leu Gly Cys Glu Asn Thr Pro Gly Ser Tyr
 370 375 380
 His Cys Thr Cys Pro Thr Gly Phe Val Leu Leu Pro Asp Gly Lys Gln
 385 390 395 400
 Cys His Glu Leu Val Ser Cys Pro Gly Asn Val Ser Lys Cys Ser His
 405 410 415
 Gly Cys Val Leu Thr Ser Asp Gly Pro Arg Cys Ile Cys Pro Ala Gly
 420 425 430
 Ser Val Leu Gly Arg Asp Gly Lys Thr Cys Thr Gly Cys Ser Ser Pro
 435 440 445
 Asp Asn Gly Gly Cys Ser Gln Ile Cys Leu Pro Leu Arg Pro Gly Ser
 450 455 460
 Trp Glu Cys Asp Cys Phe Pro Gly Tyr Asp Leu Gln Ser Asp Arg Lys
 465 470 475 480
 Ser Cys Ala Ala Ser Gly Pro Gln Pro Leu Leu Leu Phe Ala Asn Ser
 485 490 495
 Gln Asp Ile Arg His Met His Phe Asp Gly Thr Asp Tyr Lys Val Leu
 500 505 510
 Leu Ser Arg Gln Met Gly Met Val Phe Ala Leu Asp Tyr Asp Pro Val
 515 520 525
 Glu Ser Lys Ile Tyr Phe Ala Gln Thr Ala Leu Lys Trp Ile Glu Arg
 530 535 540
 Ala Asn Met Asp Gly Ser
 545 550

<210> 119
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 119
 Met Pro Trp Gly Arg Arg Pro Thr Trp Leu Leu Leu Ala Phe Leu Leu
 1 5 10 15
 Val Phe Leu Lys Ile Ser Ile Leu Ser Val Thr Ala Trp Gln Thr Gly
 20 25 30
 Asn Cys Gln Pro Gly Pro Leu Glu Arg Ser Glu Arg Ser Gly Thr Cys
 35 40 45
 Ala Gly Pro Ala Pro Phe Leu Val Phe Ser Gln Gly Lys Ser Ile Ser
 50 55 60
 Arg Ile Trp Ala Ile Pro Ser Val Ile Arg Val Asn Lys Arg Thr Gly
 65 70 75 80
 Gln Asn Arg Val Arg Leu Gln Gly Ser Met Leu Lys Pro Ser Ser Leu
 85 90 95
 Val Val Val His Pro Leu Ala Lys Pro Gly Ala Asp Pro Cys Leu Tyr
 100 105 110
 Arg Asn Gly Gly Cys Gln His Ile Cys Gln Glu Ser Leu Gly Thr Ala
 115 120 125
 Arg Cys Leu Cys Arg Glu Gly Phe Val Lys Ala Trp Asp Gly Lys Met
 130 135 140
 Cys Leu Pro Gln Asp Tyr Pro Ile Leu Ser Gly Glu Asn Ala His Asn
 145 150 155 160
 Cys Ala Phe

<210> 120
 <211> 376
 <212> PRT
 <213> Homo sapiens

<400> 120
 Met Pro Trp Gly Arg Arg Pro Thr Trp Leu Leu Leu Ala Phe Leu Leu
 1 5 10 15
 Val Ser Ala Glu Cys Gln Cys Leu Lys Gly Phe Ala Arg Asp Gly Asn
 20 25 30
 Leu Cys Ser Asp Ile Asp Glu Cys Val Leu Ala Arg Ser Asp Cys Pro
 35 40 45
 Ser Thr Ser Ser Arg Cys Ile Asn Thr Glu Gly Gly Tyr Val Cys Arg
 50 55 60
 Cys Ser Glu Gly Tyr Glu Gly Asp Gly Ile Ser Cys Phe Asp Ile Asp
 65 70 75 80

Glu Cys Gln Arg Gly Ala His Asn Cys Ala Glu Asn Ala Ala Cys Thr
 85 90 95
 Asn Thr Glu Gly Gly Tyr Asn Cys Thr Cys Ala Gly Arg Pro Ser Ser
 100 105 110
 Pro Gly Leu Ser Cys Pro Asp Ser Thr Ala Pro Ser Leu Leu Gly Glu
 115 120 125
 Asp Gly His His Leu Asp Arg Asn Ser Tyr Pro Gly Cys Pro Ser Ser
 130 135 140
 Tyr Asp Gly Tyr Cys Leu Asn Gly Gly Val Cys Met His Ile Glu Ser
 145 150 155 160
 Leu Asp Ser Tyr Thr Cys Asn Cys Val Ile Gly Tyr Ser Gly Asp Arg
 165 170 175
 Cys Gln Thr Arg Asp Leu Arg Trp Trp Glu Leu Arg His Ala Gly Tyr
 180 185 190
 Gly Gln Lys His Asp Ile Met Val Val Ala Val Cys Met Val Ala Leu
 195 200 205
 Val Leu Leu Leu Leu Leu Gly Met Trp Gly Thr Tyr Tyr Tyr Arg Thr
 210 215 220
 Arg Lys Gln Leu Ser Asn Pro Pro Lys Asn Pro Cys Asp Glu Pro Ser
 225 230 235 240
 Gly Ser Val Ser Ser Ser Gly Pro Asp Ser Ser Ser Gly Ala Ala Val
 245 250 255
 Ala Ser Cys Pro Gln Pro Trp Phe Val Val Leu Glu Lys His Gln Asp
 260 265 270
 Pro Lys Asn Gly Ser Leu Pro Ala Asp Gly Thr Asn Gly Ala Val Val
 275 280 285
 Asp Ala Gly Leu Ser Pro Ser Leu Gln Leu Gly Ser Val His Leu Thr
 290 295 300
 Ser Trp Arg Gln Lys Pro His Ile Asp Gly Met Gly Thr Gly Gln Ser
 305 310 315 320
 Cys Trp Ile Pro Pro Ser Ser Asp Arg Gly Pro Gln Glu Ile Glu Gly
 325 330 335
 Asn Ser His Leu Pro Ser Tyr Arg Pro Val Gly Pro Glu Lys Leu His
 340 345 350
 Ser Leu Gln Ser Ala Asn Gly Ser Cys His Glu Arg Ala Pro Asp Leu
 355 360 365
 Pro Arg Gln Thr Glu Pro Val Gln
 370 375

<210> 121

<211> 444

<212> PRT

<213> Homo sapiens

<400> 121

Met Pro Trp Gly Arg Lys Ala Trp Asp Gly Lys Met Cys Leu Pro Gln
 1 5 10 15
 Asp Tyr Pro Ile Leu Ser Gly Glu Asn Ala Asp Leu Ser Lys Glu Val
 20 25 30
 Thr Ser Leu Ser Asn Ser Thr Gln Ala Glu Val Pro Asp Asp Asp Gly
 35 40 45
 Thr Glu Ser Ser Thr Leu Val Ala Glu Ile Met Val Ser Gly Met Asn
 50 55 60
 Tyr Glu Asp Asp Cys Gly Pro Gly Gly Cys Gly Ser His Ala Arg Cys
 65 70 75 80
 Val Ser Asp Gly Glu Thr Ala Glu Cys Gln Cys Leu Lys Gly Phe Ala
 85 90 95
 Arg Asp Gly Asn Leu Cys Ser Asp Ile Asp Glu Cys Val Leu Ala Arg
 100 105 110
 Ser Asp Cys Pro Ser Thr Ser Ser Arg Cys Ile Asn Thr Glu Gly Gly
 115 120 125
 Tyr Val Cys Arg Cys Ser Glu Gly Tyr Glu Gly Asp Gly Ile Ser Cys
 130 135 140
 Phe Asp Ile Asp Glu Cys Gln Arg Gly Ala His Asn Cys Ala Glu Asn
 145 150 155 160
 Ala Ala Cys Thr Asn Thr Glu Gly Gly Tyr Asn Cys Thr Cys Ala Gly
 165 170 175
 Arg Pro Ser Ser Pro Gly Leu Ser Cys Pro Asp Ser Thr Ala Pro Ser
 180 185 190
 Leu Leu Gly Glu Asp Gly His His Leu Asp Arg Asn Ser Tyr Pro Gly
 195 200 205
 Cys Pro Ser Ser Tyr Asp Gly Tyr Cys Leu Asn Gly Gly Val Cys Met
 210 215 220
 His Ile Glu Ser Leu Asp Ser Tyr Thr Cys Asn Cys Val Ile Gly Tyr
 225 230 235 240
 Ser Gly Asp Arg Cys Gln Thr Arg Asp Leu Arg Trp Trp Glu Leu Arg
 245 250 255
 His Ala Gly Tyr Gly Gln Lys His Asp Ile Met Val Val Ala Val Cys
 260 265 270
 Met Val Ala Leu Val Leu Leu Leu Leu Gly Met Trp Gly Thr Tyr
 275 280 285
 Tyr Tyr Arg Thr Arg Lys Gln Leu Ser Asn Pro Pro Lys Asn Pro Cys
 290 295 300
 Asp Glu Pro Ser Gly Ser Val Ser Ser Ser Gly Pro Asp Ser Ser Ser

305 310 315 320
 Gly Ala Ala Val Ala Ser Cys Pro Gln Pro Trp Phe Val Val Leu Glu
 325 330 335
 Lys His Gln Asp Pro Lys Asn Gly Ser Leu Pro Ala Asp Gly Thr Asn
 340 345 350
 Gly Ala Val Val Asp Ala Gly Leu Ser Pro Ser Leu Gln Leu Gly Ser
 355 360 365
 Val His Leu Thr Ser Trp Arg Gln Lys Pro His Ile Asp Gly Met Gly
 370 375 380
 Thr Gly Gln Ser Cys Trp Ile Pro Pro Ser Ser Asp Arg Gly Pro Gln
 385 390 395 400
 Glu Ile Glu Gly Asn Ser His Leu Pro Ser Tyr Arg Pro Val Gly Pro
 405 410 415
 Glu Lys Leu His Ser Leu Gln Ser Ala Asn Gly Ser Cys His Glu Arg
 420 425 430
 Ala Pro Asp Leu Pro Arg Gln Thr Glu Pro Val Gln
 435 440

<210> 122
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 122
 Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala His Ala
 1 5 10 15
 Thr Glu Glu Ser Gly Asp Ser Arg Ala His Ser Ser Tyr Leu Lys Thr
 20 25 30
 Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Thr Met Val Lys Lys
 35 40 45
 Val Gly Pro Asp Ser Asp
 50

<210> 123
 <211> 855
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val
 1 5 10 15
 Val Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe
 20 25 30
 Val Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn
 35 40 45

Thr Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp
 50 55 60
 Val Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile
 65 70 75 80
 Leu Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu
 85 90 95
 Val Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly
 100 105 110
 Met Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser
 115 120 125
 Leu Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro
 130 135 140
 Phe Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr
 145 150 155 160
 Val Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val
 165 170 175
 Met Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met
 180 185 190
 Phe Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly
 195 200 205
 Lys Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu
 210 215 220
 Leu Trp Ala Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg
 225 230 235 240
 Gly Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val
 245 250 255
 Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln
 260 265 270
 Glu Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln
 275 280 285
 Arg Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn
 290 295 300
 Gly Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr
 305 310 315 320
 His Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser
 325 330 335
 Leu Lys Met Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu
 340 345 350
 Asn Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly
 355 360 365
 Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys

370	375	380																	
Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu																			
385		390				395													400
Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile																			
		405					410												415
Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp																			
		420					425												430
Asn Met Ala Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala																			
		435					440												445
Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His																			
		450					455												460
Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg																			
		465					470												480
Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro																			
							485												495
Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val																			
		500																	510
Leu Lys Met Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val																			
		515					520												525
Ser Ser Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly																			
		530					535												540
Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly																			
		545					550												560
Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro																			
							565												575
Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg																			
		580																	590
Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser																			
		595																	605
Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro																			
		610					615												620
Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro																			
		625					630												640
Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg																			
							645												655
Ser Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu																			
		660																	670
Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu																			
		675																	685
Leu His Ala Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu																			
		690					695												700

Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala
 705 710 715 720
 Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys
 725 730 735
 Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu
 740 745 750
 Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg
 755 760 765
 Gln His Val Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly
 770 775 780
 Ala Val Cys Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu
 785 790 795 800
 Ser Gly Ala Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu
 805 810 815
 Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Xaa Val
 820 825 830
 Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile
 835 840 845
 Ser Ser Leu Glu Ser Glu Val
 850 855

<210> 124
 <211> 665
 <212> PRT
 <213> Homo sapiens

<400> 124
 Met Arg Leu Ala Val Gly Ala Leu Leu Val Cys Ala Val Leu Gly Leu
 1 5 10 15
 Cys Leu Ala Val Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu
 20 25 30
 His Glu Ala Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val
 35 40 45
 Ile Pro Ser Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr
 50 55 60
 Leu Asp Cys Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr
 65 70 75 80
 Leu Asp Ala Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu
 85 90 95
 Lys Pro Val Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr
 100 105 110
 Phe Tyr Tyr Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met
 115 120 125

Asn Gln Leu Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
 130 135 140
 Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu
 145 150 155 160
 Pro Arg Lys Pro Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser
 165 170 175
 Cys Ala Pro Cys Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu
 180 185 190
 Cys Pro Gly Cys Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser
 195 200 205
 Gly Ala Phe Lys Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val
 210 215 220
 Lys His Ser Thr Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp
 225 230 235 240
 Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu
 245 250 255
 Tyr Lys Asp Cys His Leu Ala Gln Val Pro Ser His Thr Val Val Ala
 260 265 270
 Arg Ser Met Gly Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn Gln
 275 280 285
 Ala Gln Glu His Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu Phe
 290 295 300
 Ser Ser Pro His Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His Gly
 305 310 315 320
 Phe Leu Lys Val Pro Pro Arg Met Asp Ala Lys Met Tyr Leu Gly Tyr
 325 330 335
 Glu Tyr Val Thr Ala Ile Arg Asn Leu Arg Glu Gly Thr Cys Pro Glu
 340 345 350
 Ala Pro Thr Asp Glu Cys Lys Pro Val Lys Trp Cys Ala Leu Ser His
 355 360 365
 His Glu Arg Leu Lys Cys Asp Glu Trp Ser Val Asn Ser Val Gly Lys
 370 375 380
 Ile Glu Cys Val Ser Ala Glu Thr Thr Glu Asp Cys Ile Ala Lys Ile
 385 390 395 400
 Met Asn Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Phe Val Tyr
 405 410 415
 Ile Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Asn
 420 425 430
 Lys Ser Asp Asn Cys Glu Asp Thr Pro Glu Ala Gly Tyr Phe Ala Val
 435 440 445

Ala Val Val Lys Lys Ser Ala Ser Asp Leu Thr Trp Asp Asn Leu Lys
 450 455 460

Gly Lys Lys Ser Cys His Thr Ala Phe Gly Arg Thr Ala Gly Trp Asn
 465 470 475 480

Ile Pro Met Gly Leu Leu Tyr Asn Lys Ile Asn His Cys Arg Phe Asp
 485 490 495

Glu Phe Phe Ser Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser
 500 505 510

Leu Cys Lys Leu Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn
 515 520 525

Asn Lys Glu Gly Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val
 530 535 540

Glu Lys Gly Asp Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn
 545 550 555 560

Thr Gly Gly Lys Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys
 565 570 575

Asp Tyr Glu Leu Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu
 580 585 590

Tyr Ala Asn Cys His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr
 595 600 605

Arg Lys Asp Lys Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln
 610 615 620

His Leu Phe Gly Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu
 625 630 635 640

Phe Arg Ser Glu Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr His Leu
 645 650 655

Leu Glu Ala Cys Thr Phe Arg Arg Pro ;
 660 665

<210> 125

<211> 646

<212> PRT

<213> Homo sapiens

<400> 125

Met Arg Leu Ala Val Gly Ala Leu Leu Val Cys Ala Val Leu Gly Leu
 1 5 10 15

Cys Leu Ala Val Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu
 20 25 30

His Glu Ala Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val
 35 40 45

Ile Pro Ser Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr
 50 55 60

Leu Asp Cys Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr
 65 70 75 80
 Leu Asp Ala Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu
 85 90 95
 Lys Pro Val Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr
 100 105 110
 Phe Tyr Tyr Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met
 115 120 125
 Asn Gln Leu Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
 130 135 140
 Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu
 145 150 155 160
 Pro Arg Lys Pro Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser
 165 170 175
 Cys Ala Pro Cys Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu
 180 185 190
 Cys Pro Gly Cys Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser
 195 200 205
 Gly Ala Phe Lys Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val
 210 215 220
 Lys His Ser Thr Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp
 225 230 235 240
 Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu
 245 250 255
 Tyr Lys Asp Cys His Leu Ala Gln Val Pro Ser His Thr Val Val Ala
 260 265 270
 Arg Ser Met Gly Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn Gln
 275 280 285
 Ala Gln Glu His Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu Phe
 290 295 300
 Ser Ser Pro His Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His Gly
 305 310 315 320
 Phe Leu Lys Val Pro Pro Arg Met Asp Ala Lys Met Tyr Leu Gly Tyr
 325 330 335
 Glu Tyr Val Thr Ala Ile Arg Asn Leu Arg Glu Gly Thr Cys Pro Glu
 340 345 350
 Ala Pro Thr Asp Glu Cys Lys Pro Val Lys Trp Cys Ala Leu Ser His
 355 360 365
 His Glu Arg Leu Lys Cys Asp Glu Trp Ser Val Asn Ser Val Gly Lys
 370 375 380
 Ile Glu Cys Val Ser Ala Glu Thr Thr Glu Asp Cys Ile Ala Lys Ile

385 390 395 400
 Met Asn Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Phe Val Tyr
 405 410 415
 Ile Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Asn
 420 425 430
 Lys Ser Asp Asn Cys Glu Asp Thr Pro Glu Ala Gly Tyr Phe Ala Glu
 435 440 445
 Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser Leu Cys Lys Leu
 450 455 460
 Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn Asn Lys Glu Gly
 465 470 475 480
 Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val Glu Lys Gly Asp
 485 490 495
 Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn Thr Gly Gly Lys
 500 505 510
 Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys Asp Tyr Glu Leu
 515 520 525
 Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu Tyr Ala Asn Cys
 530 535 540
 His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr Arg Lys Asp Lys
 545 550 555 560
 Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln His Leu Phe Gly
 565 570 575
 Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu Phe Arg Ser Glu
 580 585 590
 Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys Leu Ala Lys Leu
 595 600 605
 His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu Glu Tyr Val Lys
 610 615 620
 Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser Leu Leu Glu Ala
 625 630 635 640
 Cys Thr Phe Arg Arg Pro
 645

<210> 126

<211> 4787

<212> PRT

<213> Homo sapiens

<400> 126

Met Ala Glu Gly Gly Glu Gly Gly Glu Asp Glu Ile Gln Phe Leu Arg
 1 5 10 15

Thr Glu Asp Glu Val Val Leu Gln Cys Ile Ala Thr Ile His Lys Glu

20					25					30					
Gln	Arg	Lys	Phe	Cys	Leu	Ala	Ala	Glu	Gly	Leu	Gly	Asn	Arg	Leu	Cys
		35					40					45			
Phe	Leu	Glu	Pro	Thr	Ser	Glu	Ala	Lys	Tyr	Ile	Pro	Pro	Asp	Leu	Cys
	50					55					60				
Val	Cys	Asn	Phe	Val	Leu	Glu	Gln	Ser	Leu	Ser	Val	Arg	Ala	Leu	Gln
	65					70					75				80
Glu	Met	Leu	Ala	Asn	Thr	Gly	Glu	Asn	Gly	Gly	Glu	Gly	Ala	Ala	Gln
				85					90					95	
Gly	Gly	Gly	His	Arg	Thr	Leu	Leu	Tyr	Gly	His	Ala	Val	Leu	Leu	Arg
			100					105					110		
His	Ser	Phe	Ser	Gly	Met	Tyr	Leu	Thr	Cys	Leu	Thr	Thr	Ser	Arg	Ser
		115					120					125			
Gln	Thr	Asp	Lys	Leu	Ala	Phe	Asp	Val	Gly	Leu	Arg	Glu	His	Ala	Thr
	130					135					140				
Gly	Glu	Ala	Cys	Trp	Trp	Thr	Ile	His	Pro	Ala	Ser	Lys	Gln	Arg	Ser
145					150					155					160
Glu	Gly	Glu	Lys	Val	Arg	Ile	Gly	Asp	Asp	Leu	Ile	Leu	Val	Ser	Val
				165					170					175	
Ser	Ser	Glu	Arg	Tyr	Leu	His	Leu	Ser	Val	Ser	Asn	Gly	Asn	Ile	Gln
			180					185					190		
Val	Asp	Ala	Ser	Phe	Met	Gln	Thr	Leu	Trp	Asn	Val	His	Pro	Thr	Cys
		195					200					205			
Ser	Gly	Ser	Ser	Ile	Glu	Glu	Gly	Tyr	Leu	Leu	Gly	Gly	His	Val	Val
	210					215					220				
Arg	Leu	Phe	His	Gly	His	Asp	Glu	Cys	Leu	Thr	Ile	Pro	Ser	Thr	Asp
225					230					235					240
Gln	Asn	Asp	Ser	Gln	His	Arg	Arg	Ile	Phe	Tyr	Glu	Ala	Gly	Gly	Ala
				245					250					255	
Gly	Thr	Arg	Ala	Xaa	Ser	Leu	Trp	Arg	Val	Glu	Pro	Leu	Arg	Ile	Ser
			260					265					270		
Trp	Ser	Gly	Ser	Asn	Ile	Arg	Trp	Gly	Gln	Ala	Phe	Arg	Leu	Arg	His
		275					280					285			
Leu	Thr	Thr	Gly	His	Tyr	Leu	Ala	Leu	Thr	Glu	Asp	Gln	Gly	Leu	Ile
	290					295					300				
Leu	Gln	Asp	Arg	Ala	Lys	Ser	Asp	Thr	Lys	Ser	Thr	Ala	Phe	Ser	Phe
305					310					315					320
Arg	Ala	Ser	Lys	Glu	Leu	Lys	Glu	Lys	Leu	Asp	Ser	Ser	His	Lys	Arg
				325					330					335	
Asp	Ile	Glu	Gly	Met	Gly	Val	Pro	Glu	Ile	Lys	Tyr	Gly	Asp	Ser	Val
			340					345					350		

Cys Phe Val Gln His Ile Ala Ser Gly Leu Trp Val Thr Tyr Lys Ala
 355 360 365
 Gln Asp Ala Lys Thr Ser Arg Leu Gly Pro Leu Lys Arg Lys Val Ile
 370 375 380
 Leu His Gln Glu Gly His Met Asp Asp Gly Leu Thr Leu Gln Arg Cys
 385 390 395 400
 Gln Arg Glu Glu Ser Gln Ala Ala Arg Ile Ile Arg Asn Thr Thr Ala
 405 410 415
 Leu Phe Ser Gln Phe Val Ser Gly Asn Asn Arg Thr Ala Ala Pro Ile
 420 425 430
 Thr Leu Pro Ile Glu Glu Val Leu Gln Thr Leu Gln Asp Leu Ile Ala
 435 440 445
 Tyr Phe Gln Pro Pro Glu Glu Glu Met Arg His Glu Asp Lys Gln Asn
 450 455 460
 Lys Leu Arg Ser Leu Lys Asn Arg Gln Asn Leu Phe Lys Glu Glu Gly
 465 470 475 480
 Met Leu Ala Leu Val Leu Asn Cys Ile Asp Arg Leu Asn Xaa Tyr Asn
 485 490 495
 Ser Val Ala His Phe Ala Gly Ile Ala Arg Glu Glu Ser Gly Met Ala
 500 505 510
 Trp Lys Glu Ile Leu Asn Leu Leu Tyr Lys Leu Leu Ala Ala Leu Ile
 515 520 525
 Arg Gly Asn Arg Asn Asn Cys Ala Gln Phe Ser Asn Asn Leu Asp Trp
 530 535 540
 Leu Ile Ser Lys Leu Asp Arg Leu Glu Ser Ser Ser Gly Ile Leu Glu
 545 550 555 560
 Val Leu His Cys Ile Leu Thr Glu Ser Pro Glu Ala Leu Asn Leu Ile
 565 570 575
 Ala Glu Gly His Ile Lys Ser Ile Ile Ser Leu Leu Asp Lys His Gly
 580 585 590
 Arg Asn His Lys Val Leu Asp Ile Leu Cys Ser Leu Cys Leu Cys Asn
 595 600 605
 Gly Val Ala Val Arg Ala Asn Gln Asn Leu Ile Cys Asp Asn Leu Leu
 610 615 620
 Pro Arg Arg Asn Leu Leu Leu Gln Thr Arg Leu Ile Asn Asp Val Thr
 625 630 635 640
 Ser Ile Arg Pro Asn Ile Phe Leu Gly Val Ala Glu Gly Ser Ala Gln
 645 650 655
 Tyr Lys Lys Trp Tyr Phe Glu Leu Ile Ile Asp Gln Val Asp Pro Phe
 660 665 670

Leu Thr Ala Glu Pro Thr His Leu Arg Val Gly Trp Ala Ser Ser Ser
 675 680 685
 Gly Tyr Ala Pro Xaa Pro Gly Gly Gly Glu Gly Trp Gly Gly Asn Gly
 690 695 700
 Val Gly Asp Asp Leu Tyr Ser Tyr Gly Phe Asp Gly Leu His Leu Trp
 705 710 715 720
 Ser Gly Arg Ile Pro Arg Ala Val Ala Ser Xaa Asn Gln His Leu Leu
 725 730 735
 Arg Ser Asp Asp Val Val Ser Cys Cys Leu Asp Leu Gly Cys Pro Ala
 740 745 750
 Ser His Ser Ala Ser Met Gly Ser Pro Cys Arg Gly Cys Leu Arg Asn
 755 760 765
 Phe Asn Thr Asp Gly Leu Phe Phe Pro Val Met Ser Phe Ser Ala Gly
 770 775 780
 Val Lys Val Arg Phe Leu Met Gly Gly Arg His Gly Glu Phe Lys Phe
 785 790 795 800
 Leu Pro Pro Ser Gly Tyr Ala Pro Cys Tyr Glu Ala Leu Leu Pro Lys
 805 810 815
 Glu Lys Met Arg Leu Glu Pro Val Lys Glu Tyr Lys Arg Asp Ala Asp
 820 825 830
 Gly Ile Arg Asp Leu Leu Gly Thr Thr Gln Phe Leu Ser Gln Ala Ser
 835 840 845
 Phe Ile Pro Cys Pro Val Asp Thr Ser Gln Val Ile Leu Pro Pro His
 850 855 860
 Leu Glu Lys Ile Arg Asp Arg Leu Ala Glu Asn Ile His Glu Leu Trp
 865 870 875 880
 Gly Met Asn Lys Ile Glu Leu Gly Trp Thr Phe Gly Lys Ile Arg Asp
 885 890 895
 Asp Asn Lys Arg Gln His Pro Cys Leu Val Glu Phe Ser Lys Leu Pro
 900 905 910
 Glu Thr Glu Lys Asn Tyr Asn Leu Gln Met Ser Thr Glu Thr Leu Lys
 915 920 925
 Thr Leu Leu Xaa Leu Gly Cys His Ile Ala His Val Asn Pro Ala Ala
 930 935 940
 Glu Glu Asp Leu Lys Lys Val Lys Leu Pro Lys Asn Tyr Met Met Ser
 945 950 955 960
 Asn Gly Tyr Lys Pro Ala Pro Leu Asp Leu Ser Asp Val Lys Leu Leu
 965 970 975
 Pro Pro Gln Glu Ile Leu Val Asp Lys Leu Ala Glu Asn Ala His Asn
 980 985 990
 Val Trp Ala Lys Asp Arg Ile Lys Gln Gly Trp Thr Tyr Gly Ile Gln

995	1000	1005
Gln Asp Leu Lys Asn Lys Arg Asn Pro Arg Leu Val Pro Tyr Ala Leu 1010	1015	1020
Leu Asp Glu Arg Thr Lys Lys Ser Asn Arg Asp Ser Leu Arg Glu Ala 1025	1030	1035 1040
Val Arg Thr Phe Val Gly Tyr Gly Tyr Asn Ile Glu Pro Ser Asp Gln 1045	1050	1055
Glu Leu Ala Asp Ser Ala Val Glu Lys Val Ser Ile Asp Lys Ile Arg 1060	1065	1070
Phe Phe Arg Val Glu Arg Ser Tyr Xaa Val Arg Ser Gly Lys Trp Tyr 1075	1080	1085
Phe Glu Phe Glu Val Val Thr Gly Gly Asp Met Arg Val Gly Trp Ala 1090	1095	1100
Arg Pro Gly Cys Arg Pro Asp Val Glu Leu Gly Ala Asp Asp Gln Ala 1105	1110	1115 1120
Phe Val Phe Glu Gly Asn Arg Gly Gln Arg Trp His Gln Gly Ser Gly 1125	1130	1135
Tyr Phe Gly Arg Thr Trp Gln Pro Gly Asp Val Val Gly Cys Met Ile 1140	1145	1150
Asn Leu Asp Asp Ala Ser Met Ile Phe Thr Leu Asn Gly Glu Leu Leu 1155	1160	1165
Ile Thr Asn Lys Gly Ser Glu Leu Ala Phe Ala Asp Tyr Glu Ile Glu 1170	1175	1180
Asn Gly Phe Val Pro Ile Cys Cys Leu Gly Leu Ser Gln Ile Gly Arg 1185	1190	1195 1200
Met Asn Leu Gly Thr Asp Ala Ser Thr Phe Lys Phe Tyr Thr Met Cys 1205	1210	1215
Gly Leu Gln Glu Gly Phe Glu Pro Phe Ala Val Asn Met Asn Arg Asp 1220	1225	1230
Val Ala Met Trp Phe Ser Lys Arg Leu Pro Thr Phe Val Asn Val Pro 1235	1240	1245
Lys Asp His Pro His Ile Glu Val Met Arg Ile Asp Gly Thr Met Asp 1250	1255	1260
Ser Pro Pro Cys Leu Lys Val Thr His Lys Thr Phe Gly Thr Gln Asn 1265	1270	1275 1280
Ser Asn Ala Asp Met Ile Tyr Cys Arg Leu Ser Met Pro Val Glu Cys 1285	1290	1295
His Ser Ser Phe Ser His Ser Pro Cys Leu Asp Ser Glu Ala Phe Gln 1300	1305	1310
Lys Arg Lys Gln Met Gln Glu Ile Leu Ser His Thr Thr Thr Gln Cys 1315	1320	1325

Tyr Tyr Ala Ile Arg Ile Phe Xaa Gly Gln Asp Pro Ser Cys Val Trp
 1330 1335 1340
 Val Gly Trp Val Thr Pro Asp Tyr His Leu Tyr Ser Glu Lys Phe Asp
 1345 1350 1355 1360
 Leu Asn Lys Asn Cys Thr Val Thr Val Thr Leu Gly Asp Glu Arg Gly
 1365 1370 1375
 Arg Val His Glu Ser Val Lys Arg Ser Asn Cys Tyr Met Val Trp Gly
 1380 1385 1390
 Gly Asp Ile Val Ala Ser Ser Gln Arg Ser Asn Arg Ser Asn Val Asp
 1395 1400 1405
 Leu Glu Ile Gly Cys Leu Val Asp Leu Ala Met Gly Met Leu Ser Phe
 1410 1415 1420
 Ser Ala Asn Gly Lys Glu Leu Gly Thr Cys Tyr Gln Val Glu Pro Asn
 1425 1430 1435 1440
 Thr Lys Val Phe Pro Ala Val Phe Leu Gln Pro Thr Ser Thr Ser Leu
 1445 1450 1455
 Phe Gln Phe Glu Leu Gly Lys Leu Lys Asn Ala Met Pro Leu Ser Ala
 1460 1465 1470
 Ala Ile Phe Arg Ser Glu Glu Xaa Asn Pro Val Pro Gln Cys Pro Pro
 1475 1480 1485
 Arg Leu Asp Val Gln Thr Ile Gln Pro Val Leu Trp Ser Arg Met Pro
 1490 1495 1500
 Asn Ser Phe Leu Lys Val Glu Thr Glu Arg Val Ser Glu Arg His Gly
 1505 1510 1515 1520
 Trp Val Val Gln Cys Leu Glu Pro Leu Gln Met Met Ala Leu His Ile
 1525 1530 1535
 Pro Glu Glu Asn Arg Cys Val Asp Ile Leu Glu Leu Cys Glu Gln Glu
 1540 1545 1550
 Asp Leu Met Arg Phe His Tyr His Thr Leu Arg Leu Tyr Ser Ala Val
 1555 1560 1565
 Cys Ala Leu Gly Asn Ser Arg Val Ala Tyr Ala Leu Cys Ser His Val
 1570 1575 1580
 Asp Leu Ser Gln Leu Phe Tyr Ala Ile Asp Asn Lys Tyr Leu Pro Gly
 1585 1590 1595 1600
 Leu Leu Arg Ser Gly Phe Tyr Asp Leu Leu Ile Ser Ile His Leu Ala
 1605 1610 1615
 Ser Ala Lys Glu Arg Lys Leu Met Met Lys Asn Glu Tyr Ile Ile Pro
 1620 1625 1630
 Ile Thr Ser Thr Thr Arg Asn Ile Cys Leu Phe Pro Asp Glu Ser Lys
 1635 1640 1645

Arg His Gly Leu Pro Gly Val Gly Leu Arg Thr Cys Leu Lys Pro Gly
 1650 1655 1660
 Phe Arg Phe Ser Thr Pro Cys Phe Val Val Thr Gly Glu Asp His Gln
 1665 1670 1675 1680
 Lys Gln Ser Pro Glu Ile Pro Leu Glu Ser Leu Arg Thr Lys Ala Leu
 1685 1690 1695
 Ser Met Leu Thr Glu Ala Val Gln Cys Ser Gly Ala His Ile Arg Asp
 1700 1705 1710
 Pro Val Gly Gly Ser Val Glu Phe Gln Phe Val Pro Val Leu Lys Leu
 1715 1720 1725
 Ile Gly Thr Leu Leu Val Met Gly Val Phe Asp Asp Asp Asp Val Arg
 1730 1735 1740
 Gln Ile Leu Leu Leu Ile Asp Pro Ser Val Phe Gly Glu His Ser Ala
 1745 1750 1755 1760
 Gly Thr Glu Glu Gly Ala Glu Lys Glu Glu Val Thr Gln Val Glu Glu
 1765 1770 1775
 Lys Ala Val Glu Ala Gly Glu Lys Ala Gly Lys Glu Ala Pro Val Lys
 1780 1785 1790
 Gly Leu Leu Gln Thr Arg Leu Pro Glu Ser Val Lys Leu Gln Met Cys
 1795 1800 1805
 Glu Leu Leu Ser Tyr Leu Cys Asp Cys Glu Leu Gln His Arg Val Glu
 1810 1815 1820
 Ala Ile Val Ala Phe Gly Asp Ile Tyr Val Ser Lys Leu Gln Ala Asn
 1825 1830 1835 1840
 Gln Lys Phe Arg Tyr Asn Glu Leu Met Gln Ala Leu Asn Met Ser Ala
 1845 1850 1855
 Ala Leu Thr Ala Arg Lys Thr Lys Glu Phe Arg Ser Pro Pro Gln Glu
 1860 1865 1870
 Gln Ile Asn Met Leu Leu Asn Phe Gln Leu Gly Glu Asn Cys Pro Cys
 1875 1880 1885
 Pro Glu Glu Ile Arg Glu Glu Leu Tyr Asp Phe His Glu Asp Leu Leu
 1890 1895 1900
 Leu His Cys Gly Val Pro Leu Glu Glu Glu Glu Glu Glu Glu Asp
 1905 1910 1915 1920
 Thr Ser Trp Thr Gly Lys Leu Cys Ala Leu Val Tyr Lys Ile Lys Gly
 1925 1930 1935
 Pro Pro Lys Pro Glu Lys Glu Gln Pro Thr Glu Glu Glu Glu Arg Cys
 1940 1945 1950
 Pro Thr Thr Leu Lys Glu Leu Ile Ser Gln Thr Met Ile Cys Trp Ala
 1955 1960 1965
 Gln Glu Asp Gln Ile Gln Asp Ser Glu Leu Val Arg Met Met Phe Asn

1970	1975	1980
Leu Leu Arg Arg Gln Tyr Asp Ser Ile Gly Glu Leu Leu Gln Ala Leu 1985	1990	1995 2000
Arg Lys Thr Tyr Thr Ile Ser His Thr Ser Val Ser Asp Thr Ile Asn 2005	2010	2015
Leu Leu Ala Ala Leu Gly Gln Ile Arg Ser Leu Leu Ser Val Arg Met 2020	2025	2030
Gly Lys Glu Glu Glu Leu Leu Met Ile Asn Gly Leu Gly Asp Ile Met 2035	2040	2045
Asn Asn Lys Val Phe Tyr Gln His Pro Asn Leu Met Arg Val Leu Gly 2050	2055	2060
Met His Glu Thr Val Met Glu Val Met Val Asn Val Leu Gly Thr Glu 2065	2070	2075 2080
Lys Ser Gln Ile Ala Phe Pro Lys Met Val Ala Ser Cys Cys Arg Phe 2085	2090	2095
Leu Cys Tyr Phe Cys Arg Ile Ser Arg Gln Asn Gln Lys Ala Met Phe 2100	2105	2110
Glu His Leu Ser Tyr Leu Leu Glu Asn Ser Ser Val Gly Leu Ala Ser 2115	2120	2125
Pro Ser Met Arg Gly Ser Thr Pro Leu Asp Val Ala Ala Ser Ser Val 2130	2135	2140
Met Asp Asn Asn Glu Leu Ala Leu Ser Leu Glu Glu Pro Asp Leu Glu 2145	2150	2155 2160
Lys Val Val Thr Tyr Leu Ala Gly Cys Gly Leu Gln Ser Cys Pro Met 2165	2170	2175
Leu Leu Ala Lys Gly Tyr Pro Asp Val Gly Trp Asn Pro Ile Glu Gly 2180	2185	2190
Glu Arg Tyr Leu Ser Phe Leu Arg Phe Ala Val Phe Val Asn Ser Glu 2195	2200	2205
Ser Val Glu Glu Asn Ala Ser Val Val Val Lys Leu Ile Arg Arg 2210	2215	2220
Pro Glu Cys Phe Gly Pro Ala Leu Arg Gly Glu Gly Gly Asn Gly Leu 2225	2230	2235 2240
Leu Ala Ala Met Gln Gly Ala Ile Lys Ile Ser Glu Asn Pro Ala Leu 2245	2250	2255
Asp Leu Pro Ser Gln Gly Tyr Lys Arg Glu Val Ser Thr Glu Asp Asp 2260	2265	2270
Glu Glu Glu Glu Glu Ile Val His Met Gly Asn Ala Ile Met Ser Phe 2275	2280	2285
Tyr Ser Ala Leu Ile Asp Leu Leu Gly Arg Cys Ala Pro Glu Met His 2290	2295	2300

Leu Ile Gln Thr Gly Lys Gly Glu Ala Ile Arg Ile Arg Ser Ile Leu
 2305 2310 2315 2320
 Arg Ser Leu Val Pro Thr Glu Asp Leu Val Gly Ile Ile Ser Ile Pro
 2325 2330 2335
 Leu Lys Leu Pro Ser Leu Asn Lys Asp Gly Ser Val Ser Glu Pro Asp
 2340 2345 2350
 Met Ala Xaa Asn Phe Cys Pro Asp His Lys Ala Pro Met Val Leu Phe
 2355 2360 2365
 Leu Asp Arg Val Tyr Gly Ile Lys Asp Gln Thr Phe Leu Leu His Leu
 2370 2375 2380
 Leu Glu Val Gly Phe Leu Pro Asp Leu Arg Ala Ser Ala Ser Leu Asp
 2385 2390 2395 2400
 Thr Val Ser Leu Ser Thr Thr Glu Ala Ala Leu Ala Leu Asn Arg Tyr
 2405 2410 2415
 Ile Cys Ser Ala Val Leu Pro Leu Leu Thr Arg Cys Ala Pro Leu Phe
 2420 2425 2430
 Xaa Gly Thr Glu His Cys Thr Ser Leu Ile Asp Ser Thr Leu Gln Thr
 2435 2440 2445
 Ile Tyr Arg Leu Ser Lys Gly Arg Ser Leu Thr Lys Ala Gln Arg Asp
 2450 2455 2460
 Thr Ile Glu Glu Cys Leu Leu Ala Ile Cys Asn His Leu Arg Pro Ser
 2465 2470 2475 2480
 Met Leu Gln Gln Leu Leu Arg Arg Leu Val Phe Asp Val Pro Gln Leu
 2485 2490 2495
 Asn Glu Tyr Cys Lys Met Pro Leu Lys Leu Leu Thr Asn His Tyr Glu
 2500 2505 2510
 Gln Cys Trp Lys Tyr Tyr Cys Leu Pro Ser Gly Trp Gly Ser Tyr Gly
 2515 2520 2525
 Leu Ala Val Glu Glu Glu Leu His Leu Thr Glu Lys Leu Phe Trp Gly
 2530 2535 2540
 Ile Xaa Asp Ser Leu Ser His Lys Lys Tyr Asp Pro Asp Leu Phe Arg
 2545 2550 2555 2560
 Met Ala Leu Pro Cys Leu Ser Ala Ile Ala Gly Ala Leu Pro Pro Asp
 2565 2570 2575
 Tyr Leu Asp Xaa Arg Ile Thr Ala Thr Leu Glu Lys Gln Ile Ser Val
 2580 2585 2590
 Asp Ala Asp Gly Asn Phe Asp Pro Lys Pro Ile Asn Thr Met Asn Phe
 2595 2600 2605
 Ser Leu Pro Glu Lys Leu Glu Tyr Ile Val Thr Lys Tyr Ala Glu His
 2610 2615 2620

Ser His Asp Lys Trp Ala Cys Asp Lys Ser Gln Ser Gly Trp Lys Tyr
 2625 2630 2635 2640
 Gly Ile Ser Leu Asp Glu Asn Val Lys Thr His Pro Leu Ile Arg Pro
 2645 2650 2655
 Phe Lys Thr Leu Thr Glu Lys Glu Lys Glu Ile Tyr Arg Trp Pro Ala
 2660 2665 2670
 Arg Glu Ser Leu Lys Thr Met Leu Ala Val Gly Trp Thr Val Glu Arg
 2675 2680 2685
 Thr Lys Glu Gly Glu Ala Leu Val Gln Gln Arg Glu Asn Glu Lys Leu
 2690 2695 2700
 Arg Ser Val Ser Gln Ala Asn Gln Gly Asn Ser Tyr Ser Pro Ala Pro
 2705 2710 2715 2720
 Leu Asp Leu Ser Asn Val Val Leu Ser Arg Glu Leu Gln Gly Met Val
 2725 2730 2735
 Glu Val Val Ala Glu Asn Tyr His Asn Ile Trp Ala Lys Lys Lys Lys
 2740 2745 2750
 Leu Glu Leu Glu Ser Lys Gly Gly Gly Ser His Pro Leu Leu Val Pro
 2755 2760 2765
 Tyr Asp Thr Leu Thr Ala Lys Glu Lys Phe Lys Asp Arg Glu Lys Ala
 2770 2775 2780
 Gln Asp Leu Phe Lys Phe Leu Gln Val Asn Gly Ile Ile Val Ser Arg
 2785 2790 2795 2800
 Gly Met Lys Asp Met Glu Leu Asp Ala Ser Ser Met Glu Lys Arg Phe
 2805 2810 2815
 Xaa Tyr Lys Phe Leu Lys Lys Ile Leu Lys Tyr Val Asp Ser Ala Gln
 2820 2825 2830
 Glu Phe Ile Ala His Leu Glu Ala Ile Val Ser Ser Gly Lys Thr Glu
 2835 2840 2845
 Lys Ser Pro Arg Asp Gln Glu Ile Lys Phe Phe Ala Lys Val Leu Leu
 2850 2855 2860
 Pro Leu Val Asp Gln Tyr Phe Thr Ser His Cys Leu Tyr Phe Leu Ser
 2865 2870 2875 2880
 Ser Pro Leu Lys Pro Leu Ser Ser Ser Gly Tyr Ala Ser His Lys Glu
 2885 2890 2895
 Lys Glu Met Val Ala Gly Leu Phe Cys Lys Leu Ala Ala Leu Val Arg
 2900 2905 2910
 His Arg Ile Ser Leu Phe Gly Ser Asp Ser Thr Thr Met Val Ser Cys
 2915 2920 2925
 Leu His Ile Leu Ala Gln Thr Leu Asp Thr Arg Thr Val Met Lys Ser
 2930 2935 2940
 Gly Ser Glu Leu Val Lys Ala Gly Leu Arg Ala Phe Phe Glu Asn Ala

2945	2950	2955	2960
Ala Glu Asp Leu Glu Lys Thr Ser Glu Asn Leu Lys Leu Gly Lys Phe			
2965	2970	2975	
Thr His Ser Arg Thr Gln Ile Lys Gly Val Ser Gln Asn Ile Asn Tyr			
2980	2985	2990	
Thr Thr Val Ala Leu Leu Pro Ile Leu Thr Ser Ile Phe Glu His Val			
2995	3000	3005	
Thr Gln His Gln Phe Gly Met Asp Leu Leu Leu Gly Asp Val Gln Ile			
3010	3015	3020	
Ser Cys Tyr His Ile Leu Cys Ser Leu Tyr Ser Leu Gly Thr Gly Lys			
3025	3030	3035	3040
Asn Ile Tyr Val Glu Arg Gln Arg Pro Ala Leu Gly Glu Cys Leu Ala			
3045	3050	3055	
Ser Leu Ala Ala Ala Ile Pro Val Ala Phe Leu Glu Pro Thr Leu Asn			
3060	3065	3070	
Arg Tyr Asn Pro Leu Ser Val Phe Asn Thr Lys Thr Pro Arg Glu Arg			
3075	3080	3085	
Ser Ile Leu Gly Met Pro Asp Thr Val Glu Asp Met Cys Pro Asp Ile			
3090	3095	3100	
Pro Gln Leu Glu Gly Leu Met Lys Glu Ile Asn Asp Leu Ala Glu Ser			
3105	3110	3115	3120
Gly Ala Arg Tyr Thr Glu Met Pro His Val Ile Glu Val Ile Leu Pro			
3125	3130	3135	
Met Leu Cys Asn Tyr Leu Ser Tyr Trp Trp Glu Arg Gly Pro Glu Asn			
3140	3145	3150	
Leu Pro Pro Ser Thr Gly Pro Cys Cys Thr Lys Val Thr Ser Glu His			
3155	3160	3165	
Leu Ser Leu Ile Leu Gly Asn Ile Leu Lys Ile Ile Asn Asn Asn Leu			
3170	3175	3180	
Gly Ile Asp Glu Ala Ser Trp Met Lys Arg Ile Ala Val Tyr Ala Gln			
3185	3190	3195	3200
Pro Ile Ile Ser Lys Ala Arg Pro Asp Leu Leu Arg Ser His Phe Ile			
3205	3210	3215	
Pro Thr Leu Glu Lys Leu Lys Lys Lys Ala Val Lys Thr Val Gln Glu			
3220	3225	3230	
Glu Glu Gln Leu Lys Ala Asp Gly Lys Gly Asp Thr Gln Glu Ala Glu			
3235	3240	3245	
Leu Leu Ile Leu Asp Glu Phe Ala Val Leu Cys Arg Asp Leu Tyr Ala			
3250	3255	3260	
Phe Tyr Pro Met Leu Ile Arg Tyr Val Asp Asn Asn Arg Ser Asn Trp			
3265	3270	3275	3280

Leu Lys Ser Pro Asp Ala Asp Ser Asp Gln Leu Phe Arg Met Val Ala
 3285 3290 3295
 Glu Val Phe Ile Leu Trp Cys Lys Ser His Asn Phe Lys Arg Glu Glu
 3300 3305 3310
 Gln Asn Phe Val Ile Gln Asn Glu Ile Asn Asn Leu Ala Phe Leu Thr
 3315 3320 3325
 Gly Asp Ser Lys Ser Lys Met Ser Lys Ser Gly Gly Gln Asp Gln Glu
 3330 3335 3340
 Arg Lys Lys Thr Lys Arg Arg Gly Asp Leu Tyr Ser Ile Gln Thr Ser
 3345 3350 3355 3360
 Leu Ile Val Ala Ala Leu Lys Lys Met Leu Pro Ile Gly Leu Asn Met
 3365 3370 3375
 Cys Thr Pro Gly Asp Gln Glu Leu Ile Ser Leu Ala Lys Ser Arg Tyr
 3380 3385 3390
 Ser His Arg Asp Thr Asp Glu Glu Val Arg Glu His Leu Arg Asn Asn
 3395 3400 3405
 Leu His Leu Gln Glu Lys Ser Asp Asp Pro Ala Val Lys Trp Gln Leu
 3410 3415 3420
 Asn Leu Tyr Lys Asp Val Leu Lys Ser Glu Glu Pro Phe Asn Pro Glu
 3425 3430 3435 3440
 Lys Thr Val Glu Arg Val Gln Arg Ile Ser Ala Ala Val Phe His Leu
 3445 3450 3455
 Glu Gln Val Glu Gln Pro Leu Arg Ser Lys Lys Ala Val Trp His Lys
 3460 3465 3470
 Leu Leu Ser Lys Gln Arg Lys Arg Ala Val Val Ala Cys Phe Arg Met
 3475 3480 3485
 Ala Pro Leu Tyr Asn Leu Pro Arg His Arg Ser Ile Asn Leu Phe Leu
 3490 3495 3500
 His Gly Tyr Gln Arg Phe Trp Ile Glu Thr Glu Glu Tyr Ser Phe Glu
 3505 3510 3515 3520
 Glu Lys Leu Val Gln Asp Leu Ala Lys Ser Pro Lys Val Glu Glu Glu
 3525 3530 3535
 Glu Glu Glu Glu Thr Glu Lys Gln Pro Asp Pro Leu His Gln Ile Ile
 3540 3545 3550
 Leu Tyr Phe Ser Arg Asn Ala Leu Thr Glu Arg Ser Lys Leu Glu Asp
 3555 3560 3565
 Asp Pro Leu Tyr Thr Ser Tyr Ser Ser Met Met Ala Lys Ser Cys Gln
 3570 3575 3580
 Ser Gly Glu Asp Glu Glu Glu Asp Glu Asp Lys Glu Lys Thr Phe Glu
 3585 3590 3595 3600

3605	3610	3615
His Glu Arg Gly Ala Ala Glu Met Val Leu Gln Met Ile Ser Ala Ser		
3620	3625	3630
Lys Gly Glu Met Ser Pro Met Val Val Glu Thr Leu Lys Leu Gly Ile		
3635	3640	3645
Ala Ile Leu Asn Gly Gly Asn Ala Gly Val Gln Gln Lys Met Leu Asp		
3650	3655	3660
Tyr Leu Lys Glu Lys Lys Asp Ala Gly Phe Phe Gln Ser Leu Xaa Gly		
3665	3670	3675 3680
Leu Met Gln Ser Cys Ser Val Leu Asp Leu Asn Ala Xaa Glu Arg Gln		
3685	3690	3695
Asn Lys Ala Glu Gly Leu Gly Met Val Thr Glu Glu Gly Thr Leu Ile		
3700	3705	3710
Val Arg Glu Arg Gly Glu Lys Val Leu Gln Asn Asp Glu Phe Thr Arg		
3715	3720	3725
Asp Leu Phe Arg Phe Leu Gln Leu Leu Cys Glu Gly His Asn Ser Asp		
3730	3735	3740
Phe Gln Asn Phe Leu Arg Thr Gln Met Gly Asn Thr Thr Thr Val Asn		
3745	3750	3755 3760
Val Ile Ile Ser Thr Val Asp Tyr Leu Leu Arg Leu Gln Glu Ser Ile		
3765	3770	3775
Ser Asp Phe Tyr Trp Tyr Tyr Ser Gly Lys Asp Ile Ile Asp Glu Ser		
3780	3785	3790
Gly Gln His Asn Phe Ser Lys Ala Leu Ala Val Thr Lys Gln Ile Phe		
3795	3800	3805
Asn Ser Leu Thr Glu Tyr Ile Gln Gly Pro Cys Ile Gly Asn Gln Gln		
3810	3815	3820
Ser Leu Ala His Ser Arg Leu Trp Asp Ala Val Val Gly Phe Leu His		
3825	3830	3835 3840
Val Phe Ala Asn Met Gln Met Lys Leu Ser Gln Asp Ser Ser Gln Ile		
3845	3850	3855
Glu Leu Leu Lys Glu Leu Leu Asp Leu Leu Gln Asp Met Val Val Met		
3860	3865	3870
Leu Leu Ser Leu Leu Glu Gly Asn Val Val Asn Gly Thr Ile Gly Lys		
3875	3880	3885
Gln Met Val Asp Thr Leu Val Glu Ser Ser Thr Asn Val Glu Met Ile		
3890	3895	3900
Leu Lys Phe Phe Asp Met Phe Leu Lys Leu Lys Asp Leu Thr Ser Ser		
3905	3910	3915 3920
Asp Thr Phe Lys Glu Tyr Asp Pro Asp Gly Lys Gly Ile Ile Ser Lys		

3925	3930	3935
Lys Glu Phe Gln Lys Ala Met Glu Gly Gln Lys Gln Tyr Thr Gln Ser		
3940	3945	3950
Glu Ile Asp Phe Leu Leu Ser Cys Ala Glu Ala Asp Glu Asn Asp Met		
3955	3960	3965
Phe Asn Tyr Val Asp Phe Val Asp Arg Phe His Glu Pro Ala Lys Asp		
3970	3975	3980
Ile Gly Phe Asn Val Ala Val Leu Leu Thr Asn Leu Ser Glu His Met		
3985	3990	4000
Pro Asn Asp Ser Arg Leu Lys Cys Leu Leu Asp Pro Ala Glu Ser Val		
4005	4010	4015
Leu Asn Tyr Phe Xaa Pro Tyr Leu Gly Arg Ile Glu Ile Met Gly Gly		
4020	4025	4030
Ala Lys Lys Ile Glu Arg Val Tyr Phe Glu Ile Ser Glu Ser Ser Arg		
4035	4040	4045
Thr Gln Trp Glu Lys Pro Gln Val Lys Glu Ser Lys Arg Gln Phe Ile		
4050	4055	4060
Phe Asp Val Val Asn Glu Gly Gly Glu Gln Glu Lys Met Xaa Leu Phe		
4065	4070	4075
Val Asn Phe Cys Glu Asp Thr Ile Phe Glu Met Gln Leu Ala Ser Gln		
4085	4090	4095
Ile Ser Glu Ser Asp Ser Ala Asp Arg Pro Glu Glu Glu Glu Glu Asp		
4100	4105	4110
Glu Asp Ser Ser Tyr Val Leu Glu Ile Ala Gly Glu Glu Glu Glu Asp		
4115	4120	4125
Gly Ser Leu Glu Pro Ala Ser Ala Phe Ala Met Ala Cys Ala Ser Val		
4130	4135	4140
Lys Arg Asn Val Thr Asp Phe Leu Lys Arg Ala Thr Leu Lys Asn Leu		
4145	4150	4155
Arg Lys Gln Tyr Arg Asn Val Lys Lys Met Thr Ala Lys Glu Leu Val		
4165	4170	4175
Lys Val Leu Phe Ser Phe Phe Trp Met Leu Phe Val Gly Leu Phe Gln		
4180	4185	4190
Leu Leu Phe Thr Ile Leu Gly Gly Ile Phe Gln Ile Leu Trp Ser Thr		
4195	4200	4205
Val Phe Gly Gly Gly Leu Val Glu Gly Ala Lys Asn Ile Arg Val Thr		
4210	4215	4220
Lys Ile Leu Gly Asp Met Pro Asp Pro Thr Gln Phe Gly Ile His Asp		
4225	4230	4235
Asp Thr Met Glu Ala Glu Arg Ala Glu Val Met Glu Pro Gly Ile Thr		
4245	4250	4255

Thr Glu Leu Val His Phe Ile Lys Gly Glu Lys Gly Asp Thr Asp Ile
 4260 4265 4270
 Met Ser Asp Leu Phe Gly Leu His Pro Lys Lys Glu Gly Ser Leu Lys
 4275 4280 4285
 His Gly Pro Glu Val Gly Leu Gly Asp Leu Ser Glu Ile Ile Gly Lys
 4290 4295 4300
 Asp Glu Pro Pro Thr Leu Glu Ser Thr Val Gln Lys Lys Arg Lys Ala
 4305 4310 4315 4320
 Gln Ala Ala Glu Met Lys Ala Ala Asn Glu Ala Glu Gly Lys Val Glu
 4325 4330 4335
 Ser Glu Lys Ala Asp Met Glu Asp Gly Glu Lys Glu Asp Lys Asp Lys
 4340 4345 4350
 Glu Glu Glu Gln Ala Glu Tyr Leu Trp Thr Glu Val Thr Lys Lys Lys
 4355 4360 4365
 Lys Arg Arg Cys Gly Gln Lys Val Glu Lys Pro Glu Ala Phe Thr Ala
 4370 4375 4380
 Asn Phe Phe Lys Gly Leu Glu Ile Tyr Gln Thr Lys Leu Leu His Tyr
 4385 4390 4395 4400
 Leu Ala Arg Asn Phe Tyr Asn Leu Arg Phe Leu Ala Leu Phe Val Ala
 4405 4410 4415
 Phe Ala Ile Asn Phe Ile Leu Leu Phe Tyr Lys Val Thr Glu Glu Pro
 4420 4425 4430
 Leu Glu Glu Glu Thr Glu Asp Val Ala Asn Leu Trp Asn Ser Phe Asn
 4435 4440 4445
 Asp Glu Glu Glu Glu Glu Ala Met Val Phe Phe Val Leu Gln Glu Ser
 4450 4455 4460
 Thr Gly Tyr Met Ala Pro Thr Leu Arg Ala Leu Ala Ile Ile His Thr
 4465 4470 4475 4480
 Ile Ile Ser Leu Val Cys Val Val Gly Tyr Tyr Cys Leu Lys Val Pro
 4485 4490 4495
 Leu Val Val Phe Lys Arg Glu Lys Glu Ile Ala Arg Lys Leu Glu Phe
 4500 4505 4510
 Asp Gly Leu Tyr Ile Thr Glu Gln Pro Ser Glu Asp Asp Ile Lys Gly
 4515 4520 4525
 Gln Trp Asp Xaa Leu Val Ile Asn Thr Pro Ser Phe Pro Asn Asn Tyr
 4530 4535 4540
 Trp Asp Lys Phe Val Lys Arg Lys Val Ile Asn Lys Tyr Gly Asp Leu
 4545 4550 4555 4560
 Tyr Gly Ala Glu Arg Ile Ala Glu Leu Leu Gly Leu Asp Lys Asn Ala
 4565 4570 4575

Leu Asp Phe Ser Pro Val Glu Glu Thr Lys Ala Glu Ala Ala Ser Leu
 4580 4585 4590

Val Ser Trp Leu Ser Ser Xaa Asp Met Lys Tyr His Ile Trp Lys Leu
 4595 4600 4605

Gly Val Val Phe Thr Asp Asn Ser Phe Leu Tyr Leu Ala Trp Tyr Thr
 4610 4615 4620

Thr Met Ser Val Leu Gly His Tyr Asn Asn Phe Phe Phe Ala Ala His
 4625 4630 4635 4640

Leu Leu Asp Ile Ala Met Gly Phe Lys Thr Leu Arg Thr Ile Leu Ser
 4645 4650 4655

Ser Val Thr His Asn Gly Lys Gln Leu Val Leu Thr Val Gly Leu Leu
 4660 4665 4670

Ala Val Val Val Tyr Leu Tyr Thr Val Val Ala Phe Asn Phe Phe Arg
 4675 4680 4685

Lys Phe Tyr Asn Lys Ser Glu Asp Asp Asp Glu Pro Asp Met Lys Cys
 4690 4695 4700

Asp Asp Met Met Thr Cys Tyr Leu Phe His Met Tyr Val Gly Val Arg
 4705 4710 4715 4720

Ala Gly Gly Gly Ile Gly Asp Glu Ile Glu Asp Pro Ala Gly Asp Pro
 4725 4730 4735

Tyr Glu Met Tyr Arg Ile Val Phe Asp Ile Thr Phe Phe Phe Phe Val
 4740 4745 4750

Ile Val Ile Leu Leu Ala Ile Ile Gln Gly Leu Ile Ile Asp Ala Phe
 4755 4760 4765

Gly Glu Leu Arg Asp Gln Gln Glu Gln Val Arg Glu Asp Met Glu Val
 4770 4775 4780

Met Leu Leu
 4785

<210> 127

<211> 374

<212> PRT

<213> Homo sapiens

<400> 127

Met Arg Thr Leu Leu Pro Pro Ala Leu Leu Thr Cys Trp Leu Leu Ala
 1 5 10 15

Pro Val Asn Ser Ile His Pro Glu Cys Arg Phe His Leu Glu Ile Gln
 20 25 30

Glu Glu Glu Thr Lys Cys Xaa Glu Leu Leu Arg Ser Gln Thr Glu Lys
 35 40 45

His Lys Ala Cys Ser Gly Val Trp Asp Asn Ile Thr Cys Trp Arg Pro
 50 55 60

Ala Asn Val Gly Glu Thr Val Thr Val Pro Cys Pro Lys Val Phe Ser
 65 70 75 80
 Asn Phe Tyr Ser Lys Ala Gly Asn Ile Ser Lys Asn Cys Thr Ser Asp
 85 90 95
 Gly Trp Ser Glu Thr Phe Pro Asp Phe Val Asp Ala Cys Gly Tyr Ser
 100 105 110
 Asp Pro Glu Asp Glu Ser Lys Ile Thr Phe Tyr Ile Leu Val Lys Ala
 115 120 125
 Ile Tyr Thr Leu Gly Tyr Ser Val Ser Leu Met Ser Leu Ala Thr Gly
 130 135 140
 Ser Ile Ile Leu Cys Leu Phe Arg Lys Leu His Cys Thr Arg Asn Tyr
 145 150 155 160
 Ile His Leu Asn Leu Phe Leu Ser Phe Ile Leu Arg Ala Ile Ser Val
 165 170 175
 Leu Val Lys Asp Asp Val Leu Tyr Ser Ser Ser Gly Thr Leu His Cys
 180 185 190
 Pro Asp Gln Pro Ser Ser Trp Val Gly Cys Lys Leu Ser Leu Val Phe
 195 200 205
 Leu Gln Tyr Cys Ile Met Ala Asn Phe Phe Trp Leu Leu Val Glu Gly
 210 215 220
 Leu Tyr Leu His Thr Leu Leu Val Ala Met Leu Pro Pro Arg Arg Cys
 225 230 235 240
 Phe Leu Ala Tyr Leu Leu Ile Gly Trp Gly Leu Pro Thr Val Cys Ile
 245 250 255
 Gly Ala Trp Thr Ala Ala Arg Leu Tyr Leu Glu Asp Thr Gly Cys Trp
 260 265 270
 Asp Thr Asn Asp His Ser Val Pro Trp Trp Val Ile Arg Ile Pro Ile
 275 280 285
 Leu Ile Ser Ile Ile Val Asn Phe Val Leu Phe Ile Ser Ile Ile Arg
 290 295 300
 Ile Leu Leu Gln Lys Leu Thr Ser Pro Asp Val Gly Gly Asn Asp Gln
 305 310 315 320
 Ser Gln Tyr Lys Arg Leu Ala Lys Ser Thr Leu Leu Leu Ile Pro Leu
 325 330 335
 Phe Gly Val His Tyr Met Val Phe Ala Val Phe Pro Ile Ser Ile Ser
 340 345 350
 Ser Lys Tyr Gln Ile Leu Phe Glu Leu Cys Leu Gly Ser Phe Gln Val
 355 360 365
 Gly Val Arg Arg Arg Pro
 370

<210> 128
 <211> 447
 <212> PRT
 <213> Homo sapiens

<400> 128

Met Ala Gly Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro
 1 5 10 15

Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala
 20 25 30

Met Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn
 35 40 45

Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp
 50 55 60

Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu
 65 70 75 80

Phe Arg Ile Phe Asn Pro Asp Gln Asp Met Gly Val Val Ser Arg Asn
 85 90 95

Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala
 100 105 110

Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr
 115 120 125

Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu
 130 135 140

Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu
 145 150 155 160

His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met
 165 170 175

Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu
 180 185 190

Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val
 195 200 205

Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe
 210 215 220

Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro
 225 230 235 240

Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro
 245 250 255

Thr Val Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp Asp
 260 265 270

Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile
 275 280 285

290 295 300
 Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly
 305 310 315 320
 Gly Asn Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu
 325 330 335
 Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro
 340 345 350
 Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly
 355 360 365
 Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly
 370 375 380
 Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn
 385 390 395 400
 Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser
 405 410 415
 Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser
 420 425 430
 Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
 435 440 445

<210> 129

<211> 381

<212> PRT

<213> Homo sapiens

<400> 129

Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu
 1 5 10 15
 Ala Pro Ala Gly Ala Phe Arg Asn Asp Lys Cys Gly Asp Thr Ile Lys
 20 25 30
 Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
 35 40 45
 His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
 50 55 60
 Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
 65 70 75 80
 Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn
 85 90 95
 Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Pro Val
 100 105 110
 Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
 115 120 125

130	135	140
Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser		
145	150	155 160
Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile		
	165	170 175
Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe		
	180	185 190
Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr		
	195	200 205
Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile		
	210	215 220
Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser		
	225	230 235 240
Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu		
	245	250 255
Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp		
	260	265 270
Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser		
	275	280 285
Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu		
	290	295 300
Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp		
	305	310 315 320
Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val		
	325	330 335
Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys		
	340	345 350
Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp		
	355	360 365
Trp Ile Thr Ile Lys Glu Gly Asn Lys Pro Val Val Ser		
	370	375 380

<210> 130

<211> 339

<212> PRT

<213> Homo sapiens

<400> 130

Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu
1 5 10 15

Ala Pro Ala Gly Ala Phe Arg Asn Asp Lys Cys Gly Asp Thr Ile Lys
20 25 30

35	40	45
His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr		
50	55	60
Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg		
65	70	75
Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn		
85	90	95
Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Pro Val		
100	105	110
Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu		
115	120	125
Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly		
130	135	140
Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser		
145	150	155
Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile		
165	170	175
Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe		
180	185	190
Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr		
195	200	205
Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile		
210	215	220
Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser		
225	230	235
Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu		
245	250	255
Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp		
260	265	270
Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser		
275	280	285
Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu		
290	295	300
Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp		
305	310	315
Ser Tyr Arg Glu Trp Ile Gln Val Cys Ser Ile Arg Ser Ser Leu Ser		
325	330	335
Arg Ile Glu		

<211> 1350

<212> PRT

<213> Homo sapiens

<400> 131

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu
 1 5 10 15

Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro
 20 25 30

Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu
 35 40 45

Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro
 50 55 60

Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys
 65 70 75 80

Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His
 85 90 95

Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met
 100 105 110

Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His
 115 120 125

Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe
 130 135 140

Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val Met Leu Lys
 145 150 155 160

Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile
 165 170 175

Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr Thr Val Asp
 180 185 190

Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr Leu Asp Thr
 195 200 205

Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys Ile His Ser
 210 215 220

Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu
 225 230 235 240

Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp Ile
 245 250 255

Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe
 260 265 270

Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu
 275 280 285

Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser

Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys
 305 310 315 320
 Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro
 325 330 335
 Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu
 340 345 350
 Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys
 355 360 365
 Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser
 370 375 380
 Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu
 385 390 395 400
 Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe
 405 410 415
 Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys Val Arg Asn
 420 425 430
 Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser Thr Asn Glu
 435 440 445
 Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu
 450 455 460
 Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val
 465 470 475 480
 Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp Asn Gly Met
 485 490 495
 Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val Gly Ser Leu
 500 505 510
 Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe
 515 520 525
 Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val
 530 535 540
 Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met
 545 550 555 560
 Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Phe Val Phe
 565 570 575
 Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys
 580 585 590
 Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu
 595 600 605
 Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly
 610 615 620

Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile
 625 630 635 640
 Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu
 645 650 655
 Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg
 660 665 670
 Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly
 675 680 685
 Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr
 690 695 700
 Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu
 705 710 715 720
 Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn
 725 730 735
 Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser
 740 745 750
 Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly
 755 760 765
 Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln Phe Val Gly
 770 775 780
 Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys
 785 790 795 800
 His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn
 805 810 815
 Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu
 820 825 830
 Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys
 835 840 845
 Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser
 850 855 860
 Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys
 865 870 875 880
 Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys
 885 890 895
 Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser
 900 905 910
 Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly
 915 920 925
 Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser
 930 935 940
 Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met

945	950	955	960
Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn			
965		970	975
Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn			
980	985		990
Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser			
995	1000	1005	
Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp			
1010	1015	1020	
Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu			
1025	1030	1035	1040
Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met			
1045	1050		1055
Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg			
1060	1065		1070
Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg			
1075	1080	1085	
Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr			
1090	1095	1100	
Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile			
1105	1110	1115	1120
Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val			
1125	1130		1135
Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln			
1140	1145		1150
Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn			
1155	1160	1165	
Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr			
1170	1175	1180	
Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His			
1185	1190	1195	1200
Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser			
1205	1210		1215
Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser			
1220	1225		1230
Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile			
1235	1240		1245
Asp Glu Asp Gln Met Leu Gln Glu Thr Arg Asp Asp Gln Arg Leu Val			
1250	1255	1260	
Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro Ser Gln			
1265	1270	1275	1280

Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr Ala Ser
 1285 1290 1295

Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile Ser Glu
 1300 1305 1310

His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser Thr Pro
 1315 1320 1325

Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Lys Met Pro
 1330 1335 1340

Ser Ile Glu Ser Asp Val
 1345 1350

<210> 132

<211> 455

<212> PRT

<213> Homo sapiens

<400> 132

Met Arg Thr Leu Leu Pro Pro Ala Leu Leu Thr Cys Trp Leu Leu Ala
 1 5 10 15

Pro Val Asn Ser Ile His Pro Glu Cys Arg Phe His Leu Glu Ile Gln
 20 25 30

Glu Glu Glu Thr Lys Cys Xaa Glu Leu Leu Arg Ser Gln Thr Glu Lys
 35 40 45

His Lys Ala Cys Ser Gly Val Trp Asp Asn Ile Thr Cys Trp Arg Pro
 50 55 60

Ala Asn Val Gly Glu Thr Val Thr Val Pro Cys Pro Lys Val Phe Ser
 65 70 75 80

Asn Phe Tyr Ser Lys Ala Gly Asn Ile Ser Lys Asn Cys Thr Ser Asp
 85 90 95

Gly Trp Ser Glu Thr Phe Pro Asp Phe Val Asp Ala Cys Gly Tyr Ser
 100 105 110

Asp Pro Glu Asp Glu Ser Lys Ile Thr Phe Tyr Ile Leu Val Lys Ala
 115 120 125

Ile Tyr Thr Leu Gly Tyr Ser Val Ser Leu Met Ser Leu Ala Thr Gly
 130 135 140

Ser Ile Ile Leu Cys Leu Phe Arg Lys Leu His Cys Thr Arg Asn Tyr
 145 150 155 160

Ile His Leu Asn Leu Phe Leu Ser Phe Ile Leu Arg Ala Ile Ser Val
 165 170 175

Leu Val Lys Asp Asp Val Leu Tyr Ser Ser Ser Gly Thr Leu His Cys
 180 185 190

Pro Asp Gln Pro Ser Ser Trp Val Gly Cys Lys Leu Ser Leu Val Phe
 195 200 205

Leu Gln Tyr Cys Ile Met Ala Asn Phe Phe Trp Leu Leu Val Glu Gly
 210 215 220
 Leu Tyr Leu His Thr Leu Leu Val Ala Met Leu Pro Pro Arg Arg Cys
 225 230 235 240
 Phe Leu Ala Tyr Leu Leu Ile Gly Trp Gly Leu Pro Thr Val Cys Ile
 245 250 255
 Gly Ala Trp Thr Ala Ala Arg Leu Tyr Leu Glu Asp Thr Gly Cys Trp
 260 265 270
 Asp Thr Asn Asp His Ser Val Pro Trp Trp Val Ile Arg Ile Pro Ile
 275 280 285
 Leu Ile Ser Ile Ile Val Asn Phe Val Leu Phe Ile Ser Ile Ile Arg
 290 295 300
 Ile Leu Leu Gln Lys Leu Thr Ser Pro Asp Val Gly Gly Asn Asp Gln
 305 310 315 320
 Ser Gln Tyr Lys Arg Leu Ala Lys Ser Thr Leu Leu Leu Ile Pro Leu
 325 330 335
 Phe Gly Val His Tyr Met Val Phe Ala Val Phe Pro Ile Ser Ile Ser
 340 345 350
 Ser Lys Tyr Gln Ile Leu Phe Glu Leu Cys Leu Gly Ser Phe Gln Gly
 355 360 365
 Leu Val Val Ala Val Leu Tyr Cys Phe Leu Asn Ser Glu Val Ser Ser
 370 375 380
 Trp Pro Pro Trp Asn Gln Ala Gln Val Leu Thr Cys Phe Leu Arg Cys
 385 390 395 400
 Cys Pro Ala Trp Cys Arg Ser Pro His Thr Cys Leu Ser Ser Ala Gly
 405 410 415
 Ser Ser Tyr Cys Pro Gly Pro His Ser Ser Val Ser Pro Ser Glu Asn
 420 425 430
 Pro Gln Arg His Arg Gln Thr His Ser Ser Gly Pro Ser Phe Gln Thr
 435 440 445
 Pro Pro Ser Phe Arg Pro Pro
 450 455

<210> 133

<211> 452

<212> PRT

<213> Homo sapiens

<400> 133

Met Arg Thr Leu Leu Pro Pro Ala Leu Leu Thr Cys Trp Leu Leu Ala
 1 5 10 15

Pro Val Asn Ser Ile His Pro Glu Cys Arg Phe His Leu Glu Ile Gln
 20 25 30

Glu Glu Glu Thr Lys Cys Xaa Glu Leu Leu Arg Ser Gln Thr Glu Lys
 35 40 45
 His Lys Ala Cys Ser Gly Val Trp Asp Asn Ile Thr Cys Trp Arg Pro
 50 55 60
 Ala Asn Val Gly Glu Thr Val Thr Val Pro Cys Pro Lys Val Phe Ser
 65 70 75 80
 Asn Phe Tyr Ser Lys Ala Gly Asn Ile Ser Lys Asn Cys Thr Ser Asp
 85 90 95
 Gly Trp Ser Glu Thr Phe Pro Asp Phe Val Asp Ala Cys Gly Tyr Ser
 100 105 110
 Asp Pro Glu Asp Glu Ser Lys Ile Thr Phe Tyr Ile Leu Val Lys Ala
 115 120 125
 Ile Tyr Thr Leu Gly Tyr Ser Val Ser Leu Met Ser Leu Ala Thr Gly
 130 135 140
 Ser Ile Ile Leu Cys Leu Phe Arg Lys Leu His Cys Thr Arg Asn Tyr
 145 150 155 160
 Ile His Leu Asn Leu Phe Leu Ser Phe Ile Leu Arg Ala Ile Ser Val
 165 170 175
 Leu Val Lys Asp Asp Val Leu Tyr Ser Ser Ser Gly Thr Leu His Cys
 180 185 190
 Pro Asp Gln Pro Ser Ser Trp Val Gly Cys Lys Leu Ser Leu Val Phe
 195 200 205
 Leu Gln Tyr Cys Ile Met Ala Asn Phe Phe Trp Leu Leu Val Glu Gly
 210 215 220
 Leu Tyr Leu His Thr Leu Leu Val Ala Met Leu Pro Pro Arg Arg Cys
 225 230 235 240
 Phe Leu Ala Tyr Leu Leu Ile Gly Trp Gly Leu Pro Thr Val Cys Ile
 245 250 255
 Gly Ala Trp Thr Ala Ala Arg Leu Tyr Leu Glu Asp Thr Gly Cys Trp
 260 265 270
 Asp Thr Asn Asp His Ser Val Pro Trp Trp Val Ile Arg Ile Pro Ile
 275 280 285
 Leu Ile Ser Ile Ile Val Asn Phe Val Leu Phe Ile Ser Ile Ile Arg
 290 295 300
 Ile Leu Leu Gln Lys Leu Thr Ser Pro Asp Val Gly Gly Asn Asp Gln
 305 310 315 320
 Ser Gln Tyr Lys Arg Leu Ala Lys Ser Thr Leu Leu Leu Ile Pro Leu
 325 330 335
 Phe Gly Val His Tyr Met Val Phe Ala Val Phe Pro Ile Ser Ile Ser
 340 345 350

Ser Lys Tyr Gln Ile Leu Phe Glu Leu Cys Leu Gly Ser Phe Gln Gly
 355 360 365
 Leu Val Val Ala Val Leu Tyr Cys Phe Leu Asn Ser Glu Val Ser Ser
 370 375 380
 Trp Pro Pro Trp Asn Gln Ala Gln Val Leu Thr Cys Phe Leu Arg Cys
 385 390 395 400
 Cys Pro Ala Trp Cys Arg Ser Pro His Thr Cys Leu Ser Ser Ala Gly
 405 410 415
 Ser Ser Tyr Cys Pro Gly Pro His Ser Ser Val Ser Pro Ser Glu Asn
 420 425 430
 Pro Gln Arg His Arg Gln Thr His Ser Ser Gly Trp Gly Val Gly Leu
 435 440 445
 His Ser Val Leu
 450

<210> 134
 <211> 1344
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Lys Ser Gly Ser Gly Gly Gly Ser Pro Thr Ser Leu Trp Gly Leu
 1 5 10 15
 Leu Phe Leu Ser Ala Ala Leu Ser Leu Trp Pro Thr Ser Gly Glu Ile
 20 25 30
 Cys Gly Pro Gly Ile Asp Ile Arg Asn Asp Tyr Gln Gln Leu Lys Arg
 35 40 45
 Leu Glu Asn Cys Thr Val Ile Glu Gly Tyr Leu His Ile Leu Leu Ile
 50 55 60
 Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
 65 70 75 80
 Ile Thr Glu Tyr Leu Leu Leu Phe Arg Val Ala Gly Leu Glu Ser Leu
 85 90 95
 Gly Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Trp Lys Leu Phe
 100 105 110
 Tyr Asn Tyr Ala Leu Val Ile Phe Glu Met Thr Asn Leu Lys Asp Ile
 115 120 125
 Gly Leu Tyr Asn Leu Arg Asn Ile Thr Arg Gly Ala Ile Arg Ile Glu
 130 135 140
 Lys Asn Ala Asp Leu Cys Tyr Leu Ser Thr Val Asp Trp Ser Leu Ile
 145 150 155 160
 Leu Asp Ala Val Ser Asn Asn Tyr Ile Val Gly Asn Lys Pro Pro Lys
 165 170 175

Glu Cys Gly Asp Leu Cys Pro Gly Thr Met Glu Glu Lys Pro Met Cys
 180 185 190
 Glu Lys Thr Thr Ile Asn Asn Glu Tyr Asn Tyr Arg Cys Trp Thr Thr
 195 200 205
 Asn Arg Cys Gln Lys Met Cys Pro Ser Thr Cys Gly Lys Arg Ala Cys
 210 215 220
 Thr Glu Asn Asn Glu Cys Cys His Pro Glu Cys Leu Gly Ser Cys Ser
 225 230 235 240
 Ala Pro Asp Asn Asp Thr Ala Cys Val Ala Cys Arg His Tyr Tyr Tyr
 245 250 255
 Ala Gly Val Cys Val Pro Ala Cys Pro Pro Asn Thr Tyr Arg Phe Glu
 260 265 270
 Gly Trp Arg Cys Val Asp Arg Asp Phe Cys Ala Asn Ile Leu Ser Ala
 275 280 285
 Glu Ser Ser Asp Ser Glu Gly Phe Val Ile His Asp Gly Glu Cys Met
 290 295 300
 Gln Glu Cys Pro Ser Gly Phe Ile Arg Asn Gly Ser Gln Ser Met Tyr
 305 310 315 320
 Cys Ile Pro Cys Glu Gly Pro Cys Pro Lys Val Cys Glu Glu Glu Lys
 325 330 335
 Lys Thr Lys Thr Ile Asp Ser Val Thr Ser Ala Gln Met Leu Gln Gly
 340 345 350
 Cys Thr Ile Phe Lys Gly Asn Leu Leu Ile Asn Ile Arg Arg Gly Asn
 355 360 365
 Asn Ile Ala Ser Glu Leu Glu Asn Phe Met Gly Leu Ile Glu Val Val
 370 375 380
 Thr Gly Tyr Val Lys Ile Arg His Ser His Ala Leu Val Ser Leu Ser
 385 390 395 400
 Phe Leu Lys Asn Leu Arg Leu Ile Leu Gly Glu Glu Gln Leu Glu Gly
 405 410 415
 Asn Tyr Ser Phe Tyr Val Leu Asp Asn Gln Asn Leu Gln Gln Leu Trp
 420 425 430
 Asp Trp Asp His Arg Asn Leu Thr Ile Lys Ala Gly Lys Met Tyr Phe
 435 440 445
 Ala Phe Asn Pro Lys Leu Cys Val Ser Glu Ile Tyr Arg Met Glu Glu
 450 455 460
 Val Thr Gly Thr Lys Gly Arg Gln Ser Lys Gly Asp Ile Asn Thr Arg
 465 470 475 480
 Asn Asn Gly Glu Arg Ala Ser Cys Glu Ser Asp Val Leu His Phe Thr
 485 490 495
 Ser Thr Thr Thr Ser Lys Asn Arg Ile Ile Ile Thr Trp His Arg Tyr

500					505					510					
Arg	Pro	Pro	Asp	Tyr	Arg	Asp	Leu	Ile	Ser	Phe	Thr	Val	Tyr	Tyr	Lys
		515					520					525			
Glu	Ala	Pro	Phe	Lys	Asn	Val	Thr	Glu	Tyr	Asp	Gly	Gln	Asp	Ala	Cys
		530					535					540			
Gly	Ser	Asn	Ser	Trp	Asn	Met	Val	Asp	Val	Asp	Leu	Pro	Pro	Asn	Lys
							550					555			560
Asp	Val	Glu	Pro	Gly	Ile	Leu	Leu	His	Gly	Leu	Lys	Pro	Trp	Thr	Gln
									570					575	
Tyr	Ala	Val	Tyr	Val	Lys	Ala	Val	Thr	Leu	Thr	Met	Val	Glu	Asn	Asp
									585					590	
His	Ile	Arg	Gly	Ala	Lys	Ser	Glu	Ile	Leu	Tyr	Ile	Arg	Thr	Asn	Ala
									600					605	
Ser	Val	Pro	Ser	Ile	Pro	Leu	Asp	Val	Leu	Ser	Ala	Ser	Asn	Ser	Ser
									615					620	
Ser	Gln	Leu	Ile	Val	Lys	Trp	Asn	Pro	Pro	Ser	Leu	Pro	Asn	Gly	Asn
									635					640	
Leu	Ser	Tyr	Tyr	Ile	Val	Arg	Trp	Gln	Arg	Gln	Pro	Gln	Asp	Gly	Tyr
									650					655	
Leu	Tyr	Arg	His	Asn	Tyr	Cys	Ser	Lys	Asp	Lys	Ile	Pro	Ile	Arg	Lys
									665					670	
Tyr	Ala	Asp	Gly	Thr	Ile	Asp	Ile	Glu	Glu	Val	Thr	Glu	Asn	Pro	Lys
									680					685	
Thr	Glu	Val	Cys	Gly	Gly	Glu	Lys	Gly	Pro	Cys	Cys	Ala	Cys	Pro	Lys
									695					700	
Thr	Glu	Ala	Glu	Lys	Gln	Ala	Glu	Lys	Glu	Glu	Ala	Glu	Tyr	Arg	Lys
									715					720	
Val	Phe	Glu	Asn	Phe	Leu	His	Asn	Ser	Ile	Phe	Val	Pro	Arg	Pro	Glu
									730					735	
Arg	Lys	Arg	Arg	Asp	Val	Met	Gln	Val	Ala	Asn	Thr	Thr	Met	Ser	Ser
									745					750	
Arg	Ser	Arg	Asn	Thr	Thr	Ala	Ala	Asp	Thr	Tyr	Asn	Ile	Thr	Asp	Pro
									760					765	
Glu	Glu	Leu	Glu	Thr	Glu	Tyr	Pro	Phe	Phe	Glu	Ser	Arg	Val	Asp	Asn
									775					780	
Lys	Glu	Arg	Thr	Val	Ile	Ser	Asn	Leu	Arg	Pro	Phe	Thr	Leu	Tyr	Arg
									790					800	
Ile	Asp	Ile	His	Ser	Cys	Asn	His	Glu	Ala	Glu	Lys	Leu	Gly	Cys	Ser
									810					815	
Ala	Ser	Asn	Phe	Val	Phe	Ala	Arg	Thr	Met	Pro	Ala	Glu	Gly	Ala	Asp
									825					830	

Asp Ile Pro Gly Pro Val Thr Trp Glu Pro Arg Pro Glu Asn Ser Ile
 835 840 845
 Phe Leu Lys Trp Pro Glu Pro Glu Asn Pro Asn Gly Leu Ile Leu Met
 850 855 860
 Tyr Glu Ile Lys Tyr Gly Ser Gln Val Glu Asp Gln Arg Glu Cys Val
 865 870 875 880
 Ser Arg Gln Glu Tyr Arg Lys Tyr Gly Gly Ala Lys Leu Asn Arg Leu
 885 890 895
 Asn Pro Gly Asn Tyr Thr Ala Arg Ile Gln Ala Thr Ser Leu Ser Gly
 900 905 910
 Asn Gly Ser Trp Thr Asp Pro Val Phe Phe Tyr Val Gln Ala Lys Thr
 915 920 925
 Gly Tyr Glu Asn Phe Ile His Leu Ile Ile Ala Leu Pro Val Ala Val
 930 935 940
 Leu Leu Ile Val Gly Gly Leu Val Ile Met Leu Tyr Val Phe His Arg
 945 950 955 960
 Lys Arg Asn Asn Ser Arg Leu Gly Asn Gly Val Leu Tyr Ala Ser Val
 965 970 975
 Asn Pro Glu Tyr Phe Ser Ala Ala Asp Val Tyr Val Pro Asp Glu Trp
 980 985 990
 Glu Val Ala Arg Glu Lys Ile Thr Met Ser Arg Glu Leu Gly Gln Gly
 995 1000 1005
 Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val Lys Asp
 1010 1015 1020
 Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu Ala Ala Ser
 1025 1030 1035 1040
 Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met Lys Glu
 1045 1050 1055
 Phe Asn Cys His His Val Val Arg Leu Leu Gly Val Val Ser Gln Gly
 1060 1065 1070
 Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr Arg Gly Asp Leu Lys
 1075 1080 1085
 Ser Tyr Leu Arg Ser Leu Arg Pro Glu Met Glu Asn Asn Pro Val Leu
 1090 1095 1100
 Ala Pro Pro Ser Leu Ser Lys Met Ile Gln Met Ala Gly Glu Ile Ala
 1105 1110 1115 1120
 Asp Gly Met Ala Tyr Leu Asn Ala Asn Lys Phe Val His Arg Asp Leu
 1125 1130 1135
 Ala Ala Arg Asn Cys Met Val Ala Glu Asp Phe Thr Val Lys Ile Gly
 1140 1145 1150

Asp Phe Gly Met Thr Arg Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys
 1155 1160 1165
 Gly Gly Lys Gly Leu Leu Pro Val Arg Trp Met Ser Pro Glu Ser Leu
 1170 1175 1180
 Lys Asp Gly Val Phe Thr Thr Tyr Ser Asp Val Trp Ser Phe Gly Val
 1185 1190 1195 1200
 Val Leu Trp Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu
 1205 1210 1215
 Ser Asn Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp
 1220 1225 1230
 Lys Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg Met Cys
 1235 1240 1245
 Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile Ser
 1250 1255 1260
 Ser Ile Lys Glu Glu Leu Asp Leu Glu Pro Glu Asn Met Glu Ser Val
 1265 1270 1275 1280
 Pro Leu Asp Pro Ser Ala Ser Ser Ser Ser Leu Pro Leu Pro Asp Arg
 1285 1290 1295
 His Ser Gly His Lys Ala Glu Asn Gly Pro Gly Pro Gly Val Leu Val
 1300 1305 1310
 Leu Arg Ala Ser Phe Asp Glu Arg Gln Pro Tyr Ala His Met Asn Gly
 1315 1320 1325
 Gly Arg Lys Asn Glu Arg Ala Leu Pro Leu Pro Gln Ser Ser Thr Cys
 1330 1335 1340

<210> 135
 <211> 600
 <212> PRT
 <213> Homo sapiens

<400> 135
 Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu
 1 5 10 15
 Ala Pro Ala Gly Ala Phe Arg Asn Asp Lys Cys Gly Asp Thr Ile Lys
 20 25 30
 Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
 35 40 45
 His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
 50 55 60
 Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
 65 70 75 80

Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn
 85 90 95
 Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Pro Val
 100 105 110
 Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
 115 120 125
 Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
 130 135 140
 Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser
 145 150 155 160
 Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile
 165 170 175
 Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe
 180 185 190
 Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr
 195 200 205
 Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile
 210 215 220
 Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser
 225 230 235 240
 Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu
 245 250 255
 Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp
 260 265 270
 Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser
 275 280 285
 Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu
 290 295 300
 Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp
 305 310 315 320
 Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val
 325 330 335
 Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys
 340 345 350
 Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp
 355 360 365
 Trp Ile Thr Ile Lys Glu Gly Asn Lys Pro Val Leu Phe Gln Gly Asn
 370 375 380
 Thr Asn Pro Thr Asp Val Val Val Ala Val Phe Pro Lys Pro Leu Ile
 385 390 395 400
 Thr Arg Phe Val Arg Ile Lys Pro Ala Thr Trp Glu Thr Gly Ile Ser

405 410 415
 Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser
 420 425 430
 Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr
 435 440 445
 Ser Ser Asn Gln Gly Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu
 450 455 460
 Val Thr Ser Arg Ser Gly Trp Ala Leu Pro Pro Ala Pro His Ser Tyr
 465 470 475 480
 Ile Asn Glu Trp Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile Val Arg
 485 490 495
 Gly Ile Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met
 500 505 510
 Arg Lys Phe Lys Ile Gly Tyr Ser Asn Asn Gly Ser Asp Trp Lys Met
 515 520 525
 Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn
 530 535 540
 Asn Tyr Asp Thr Pro Glu Leu Arg Thr Phe Pro Ala Leu Ser Thr Arg
 545 550 555 560
 Phe Ile Arg Ile Tyr Pro Glu Arg Ala Thr His Gly Gly Leu Gly Leu
 565 570 575
 Arg Met Glu Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro
 580 585 590
 Thr Thr Pro Asn Gly Asn Leu Val
 595 600

 <210> 136
 <211> 840
 <212> PRT
 <213> Homo sapiens

 <400> 136
 Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu
 1 5 10 15
 Ala Pro Ala Gly Ala Phe Arg Asn Asp Lys Cys Gly Asp Thr Ile Lys
 20 25 30
 Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
 35 40 45
 His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
 50 55 60
 Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
 65 70 75 80
 Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn

85				90				95							
Gly	His	Phe	Arg 100	Gly	Lys	Phe	Cys	Gly	Lys	Ile	Ala	Pro	Pro	Pro	Val
Val	Ser	Ser	Gly 115	Pro	Phe	Leu	Phe	Ile	Lys	Phe	Val	Ser	Asp	Tyr	Glu
Thr	His	Gly	Ala	Gly	Phe	Ser	Ile	Arg	Tyr	Glu	Ile	Phe	Lys	Arg	Gly
Pro	Glu	Cys	Ser	Gln	Asn	Tyr	Thr	Thr	Pro	Ser	Gly	Val	Ile	Lys	Ser
Pro	Gly	Phe	Pro	Glu	Lys	Tyr	Pro	Asn	Ser	Leu	Glu	Cys	Thr	Tyr	Ile
Val	Phe	Ala	Pro	Lys	Met	Ser	Glu	Ile	Ile	Leu	Glu	Phe	Glu	Ser	Phe
Asp	Leu	Glu	Pro	Asp	Ser	Asn	Pro	Pro	Gly	Gly	Met	Phe	Cys	Arg	Tyr
Asp	Arg	Leu	Glu	Ile	Trp	Asp	Gly	Phe	Pro	Asp	Val	Gly	Pro	His	Ile
Gly	Arg	Tyr	Cys	Gly	Gln	Lys	Thr	Pro	Gly	Arg	Ile	Arg	Ser	Ser	Ser
Gly	Ile	Leu	Ser	Met	Val	Phe	Tyr	Thr	Asp	Ser	Ala	Ile	Ala	Lys	Glu
Gly	Phe	Ser	Ala	Asn	Tyr	Ser	Val	Leu	Gln	Ser	Ser	Val	Ser	Glu	Asp
Phe	Lys	Cys	Met	Glu	Ala	Leu	Gly	Met	Glu	Ser	Gly	Glu	Ile	His	Ser
Asp	Gln	Ile	Thr	Ala	Ser	Ser	Gln	Tyr	Ser	Thr	Asn	Trp	Ser	Ala	Glu
Arg	Ser	Arg	Leu	Asn	Tyr	Pro	Glu	Asn	Gly	Trp	Thr	Pro	Gly	Glu	Asp
Ser	Tyr	Arg	Glu	Trp	Ile	Gln	Val	Asp	Leu	Gly	Leu	Leu	Arg	Phe	Val
Thr	Ala	Val	Gly	Thr	Gln	Gly	Ala	Ile	Ser	Lys	Glu	Thr	Lys	Lys	Lys
Tyr	Tyr	Val	Lys	Thr	Tyr	Lys	Ile	Asp	Val	Ser	Ser	Asn	Gly	Glu	Asp
Trp	Ile	Thr	Ile	Lys	Glu	Gly	Asn	Lys	Pro	Val	Leu	Phe	Gln	Gly	Asn
Thr	Asn	Pro	Thr	Asp	Val	Val	Val	Ala	Val	Phe	Pro	Lys	Pro	Leu	Ile
Thr	Arg	Phe	Val	Arg	Ile	Lys	Pro	Ala	Thr	Trp	Glu	Thr	Gly	Ile	Ser

Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser
 420 425 430
 Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr
 435 440 445
 Ser Ser Asn Gln Gly Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu
 450 455 460
 Val Thr Ser Arg Ser Gly Trp Ala Leu Pro Pro Ala Pro His Ser Tyr
 465 470 475 480
 Ile Asn Glu Trp Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile Val Arg
 485 490 495
 Gly Ile Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met
 500 505 510
 Arg Lys Phe Lys Ile Gly Tyr Ser Asn Asn Gly Ser Asp Trp Lys Met
 515 520 525
 Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Gly Gly Thr Thr Val Leu
 530 535 540
 Ala Thr Glu Lys Pro Thr Val Ile Asp Ser Thr Ile Gln Ser Glu Phe
 545 550 555 560
 Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser His Lys Thr
 565 570 575
 Phe Cys His Trp Glu His Asp Asn His Val Gln Leu Lys Trp Ser Val
 580 585 590
 Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly Asp Gly Asn
 595 600 605
 Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys Val Ala Arg
 610 615 620
 Leu Val Ser Pro Val Val Tyr Ser Gln Asn Ser Ala His Cys Met Thr
 625 630 635 640
 Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu Arg Val Lys
 645 650 655
 Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val Trp Met Ala
 660 665 670
 Ile Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val Leu Leu His
 675 680 685
 Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu Ile Gly Lys
 690 695 700
 Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile Asn Asn His
 705 710 715 720
 Ile Ser Gln Glu Asp Cys Ala Lys Pro Ala Asp Leu Asp Lys Lys Asn
 725 730 735

ro Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly Tyr Glu Gly
 740 745 750
 lu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly Asn Val Leu
 755 760 765
 ys Thr Leu Xaa Pro Ile Leu Ile Thr Ile Ile Ala Met Ser Ala Leu
 770 775 780
 ly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr Cys Ala Cys
 785 790 795 800
 rp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu Glu Asn Tyr
 805 810 815
 Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp Lys Leu Asn
 820 825 830
 Thr Gln Ser Thr Tyr Ser Glu Ala
 835 840

<210> 137
 <211> 538
 <212> PRT
 <213> Homo sapiens

<400> 137

Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu
 1 5 10 15
 Ala Pro Ala Gly Ala Phe Arg Asn Asp Lys Cys Gly Asp Thr Ile Lys
 20 25 30
 Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
 35 40 45
 His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
 50 55 60
 Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
 65 70 75 80
 Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn
 85 90 95
 Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Pro Val
 100 105 110
 Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
 115 120 125
 Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
 130 135 140
 Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser
 145 150 155 160
 Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile
 165 170 175

Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe
 180 185 190
 Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr
 195 200 205
 Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile
 210 215 220
 Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser
 225 230 235 240
 Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu
 245 250 255
 Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp
 260 265 270
 Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser
 275 280 285
 Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu
 290 295 300
 Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp
 305 310 315 320
 Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val
 325 330 335
 Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys
 340 345 350
 Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp
 355 360 365
 Trp Ile Thr Ile Lys Glu Gly Asn Lys Pro Val Leu Phe Gln Gly Asn
 370 375 380
 Thr Asn Pro Thr Asp Val Val Val Ala Val Phe Pro Lys Pro Leu Ile
 385 390 395 400
 Thr Arg Phe Val Arg Ile Lys Pro Ala Thr Trp Glu Thr Gly Ile Ser
 405 410 415
 Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser
 420 425 430
 Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr
 435 440 445
 Ser Ser Asn Gln Gly Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu
 450 455 460
 Val Thr Ser Arg Ser Gly Trp Ala Leu Pro Pro Ala Pro His Ser Tyr
 465 470 475 480
 Ile Asn Glu Trp Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile Val Arg
 485 490 495
 Gly Ile Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met

500							505				510				
Arg	Lys	Phe	Lys	Ile	Gly	Tyr	Ser	Asn	Asn	Gly	Ser	Asp	Trp	Lys	Met
515							520				525				
Ile	Met	Asp	Asp	Ser	Lys	Arg	Lys	Ala	Arg						
530							535								

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<210> 138
<211> 389
<212> PRT
<213> Homo sapiens
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<400> 138															
Met	Gly	Ala	Pro	Ala	Cys	Ala	Leu	Ala	Leu	Cys	Val	Ala	Val	Ala	Ile
1				5					10					15	
Val	Ala	Gly	Ala	Ser	Ser	Glu	Ser	Leu	Gly	Thr	Glu	Gln	Arg	Val	Val
			20					25					30		
Gly	Arg	Ala	Ala	Glu	Val	Pro	Gly	Pro	Glu	Pro	Gly	Gln	Gln	Glu	Gln
		35					40					45			
Leu	Val	Phe	Gly	Ser	Gly	Asp	Ala	Val	Glu	Leu	Ser	Cys	Pro	Pro	Pro
	50					55					60				
Gly	Gly	Gly	Pro	Met	Gly	Pro	Thr	Val	Trp	Val	Lys	Asp	Gly	Thr	Gly
65					70					75					80
Leu	Val	Pro	Ser	Glu	Arg	Val	Leu	Val	Gly	Pro	Gln	Arg	Leu	Gln	Val
				85					90					95	
Leu	Asn	Ala	Ser	His	Glu	Asp	Ser	Gly	Ala	Tyr	Ser	Cys	Arg	Gln	Arg
		100						105					110		
Leu	Thr	Gln	Arg	Val	Leu	Cys	His	Phe	Ser	Val	Arg	Val	Thr	Asp	Ala
		115					120					125			
Pro	Ser	Ser	Gly	Asp	Asp	Glu	Asp	Gly	Glu	Asp	Glu	Ala	Glu	Asp	Thr
	130					135					140				
Gly	Val	Asp	Thr	Gly	Ala	Pro	Tyr	Trp	Thr	Arg	Pro	Glu	Arg	Met	Asp
145					150					155					160
Lys	Lys	Leu	Leu	Ala	Val	Pro	Ala	Ala	Asn	Thr	Val	Arg	Phe	Arg	Cys
				165					170					175	
Pro	Ala	Ala	Gly	Asn	Pro	Thr	Pro	Ser	Ile	Ser	Trp	Leu	Lys	Asn	Gly
			180					185					190		
Arg	Glu	Phe	Arg	Gly	Glu	His	Arg	Ile	Gly	Gly	Ile	Lys	Leu	Arg	His
		195					200					205			
Gln	Gln	Trp	Ser	Leu	Val	Met	Glu	Ser	Val	Val	Pro	Ser	Asp	Arg	Gly
	210					215					220				
Asn	Tyr	Thr	Cys	Val	Val	Glu	Asn	Lys	Phe	Gly	Ser	Ile	Arg	Gln	Thr
225					230					235					240
Tyr	Thr	Leu	Asp	Val	Leu	Glu	Arg	Ser	Pro	His	Arg	Pro	Ile	Leu	Gln

[illegible]

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<210> 139
<211> 330
<212> PRT
<213> Mouse
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<400> 139

Met	Thr	Leu	Arg	His	Leu	Pro	Phe	Ile	Leu	Leu	Ile	Leu	Ser	Gly			
1				5					10					15			
Glu	Leu	Tyr	Ala	Glu	Glu	Lys	Gln	Cys	Asp	Phe	Pro	Thr	Val	Glu	Asn		
			20					25					30				
Gly	Arg	Ile	Ala	Gln	Tyr	Tyr	Tyr	Thr	Phe	Lys	Ser	Phe	Tyr	Phe	Pro		
		35					40					45					
Met	Ser	Val	Asp	Lys	Lys	Leu	Ser	Phe	Phe	Cys	Leu	Ala	Gly	Tyr	Ala		
	50					55					60						
Thr	Glu	Ser	Gly	Lys	Gln	Glu	Glu	Gln	Ile	Arg	Cys	Thr	Ala	Glu	Gly		
65					70					75					80		
Trp	Ser	Pro	Asn	Pro	Arg	Cys	Tyr	Lys	Lys	Cys	Leu	Lys	Pro	Asp	Leu		
				85					90					95			
Arg	Asn	Gly	Tyr	Val	Ser	Asn	Asp	Lys	Val	Leu	Tyr	Lys	Leu	Gln	Glu		
		100						105					110				
Arg	Met	Ser	Tyr	Gly	Cys	Ser	Ser	Gly	Tyr	Lys	Thr	Thr	Gly	Gly	Lys		
	115						120					125					
Asp	Glu	Glu	Val	Val	His	Cys	Leu	Ser	Ala	Gly	Trp	Ser	Ser	Gln	Pro		

130 135 140
 Ser Cys Arg Lys Glu Gln Glu Thr Cys Leu Ala Pro Glu Leu Glu His
 145 150 155 160
 Gly Asn Tyr Ser Thr Thr Gln Arg Thr Phe Lys Val Lys Asp Ile Val
 165 170 175
 Ala Tyr Thr Cys Thr Ala Gly Tyr Tyr Thr Thr Thr Gly Lys Gln Thr
 180 185 190
 Gly Glu Ala Glu Cys Gln Ala Asn Gly Trp Ser Leu Thr Pro Gln Cys
 195 200 205
 Asn Lys Leu Met Cys Ser Ser Leu Arg Leu Ile Glu Asn Gly Tyr Phe
 210 215 220
 His Pro Val Lys Gln Thr Tyr Glu Glu Gly Asp Val Val Gln Phe Phe
 225 230 235 240
 Cys His Glu Asn Tyr Tyr Leu Ser Gly Ser Asp Leu Ile Gln Cys Tyr
 245 250 255
 Asn Phe Gly Trp Tyr Pro Glu Ser Pro Ile Cys Glu Gly Arg Arg Asn
 260 265 270
 Arg Cys Pro Pro Pro Pro Val Pro Leu Asn Ser Lys Ile Gln Pro His
 275 280 285
 Ser Thr Thr Tyr Arg His Gly Glu Arg Val His Ile Glu Cys Glu Leu
 290 295 300
 Asn Phe Val Ile Gln Gly Ser Glu Glu Leu Leu Cys Glu Asn Gly Lys
 305 310 315 320
 Trp Thr Glu Pro Pro Lys Cys Ile Gly Trp
 325 330

<210> 140
 <211> 1073
 <212> PRT
 <213> Mouse

<400> 140

Met Pro Trp Gly Arg Arg Pro Thr Trp Leu Leu Leu Ala Phe Leu Leu
 1 5 10 15
 Val Phe Leu Lys Ile Ser Ile Leu Ser Val Thr Ala Trp Gln Thr Gly
 20 25 30
 Asn Cys Gln Pro Gly Pro Leu Glu Arg Ser Glu Arg Ser Gly Thr Cys
 35 40 45
 Ala Gly Pro Ala Pro Phe Leu Val Phe Ser Gln Gly Lys Ser Ile Ser
 50 55 60
 Arg Ile Asp Pro Asp Gly Thr Asn His Gln Gln Leu Val Val Asp Ala
 65 70 75 80
 Gly Ile Ser Ala Asp Met Asp Ile His Tyr Lys Lys Glu Arg Leu Tyr

85										90					95				
Trp	Val	Asp	Val	Glu	Arg	Gln	Val	Leu	Leu	Arg	Val	Phe	Leu	Asn	Gly				
			100					105					110						
Thr	Gly	Leu	Glu	Lys	Val	Cys	Asn	Val	Glu	Arg	Lys	Val	Ser	Gly	Leu				
		115					120					125							
Ala	Ile	Asp	Trp	Ile	Asp	Asp	Glu	Val	Leu	Trp	Val	Asp	Gln	Gln	Asn				
		130				135					140								
Gly	Val	Ile	Thr	Val	Thr	Asp	Met	Thr	Gly	Lys	Asn	Ser	Arg	Val	Leu				
145					150					155					160				
Leu	Ser	Ser	Leu	Lys	His	Pro	Ser	Asn	Ile	Ala	Val	Asp	Pro	Ile	Glu				
				165					170					175					
Arg	Leu	Met	Phe	Trp	Ser	Ser	Glu	Val	Thr	Gly	Ser	Leu	His	Arg	Ala				
			180					185					190						
His	Leu	Lys	Gly	Val	Asp	Val	Lys	Thr	Leu	Leu	Glu	Thr	Gly	Gly	Ile				
		195					200					205							
Ser	Val	Leu	Thr	Leu	Asp	Val	Leu	Asp	Lys	Arg	Leu	Phe	Trp	Val	Gln				
	210					215					220								
Asp	Ser	Gly	Glu	Gly	Ser	His	Ala	Tyr	Ile	His	Ser	Cys	Asp	Tyr	Glu				
225					230					235					240				
Gly	Gly	Ser	Val	Arg	Leu	Ile	Arg	His	Gln	Ala	Arg	His	Ser	Leu	Ser				
				245					250					255					
Ser	Met	Ala	Phe	Phe	Gly	Asp	Arg	Ile	Phe	Tyr	Ser	Val	Leu	Lys	Ser				
			260					265					270						
Lys	Ala	Ile	Trp	Ile	Ala	Asn	Lys	His	Thr	Gly	Lys	Asp	Thr	Val	Arg				
		275					280					285							
Ile	Asn	Leu	His	Pro	Ser	Phe	Val	Thr	Pro	Gly	Lys	Leu	Met	Val	Val				
	290					295					300								
His	Pro	Arg	Ala	Gln	Pro	Arg	Thr	Glu	Asp	Ala	Ala	Lys	Asp	Pro	Asp				
305					310					315					320				
Pro	Glu	Leu	Leu	Lys	Gln	Arg	Gly	Arg	Pro	Cys	Arg	Phe	Gly	Leu	Cys				
				325					330					335					
Glu	Arg	Asp	Pro	Lys	Ser	His	Ser	Ser	Ala	Cys	Ala	Glu	Gly	Tyr	Thr				
			340					345					350						
Leu	Ser	Arg	Asp	Arg	Lys	Tyr	Cys	Glu	Asp	Val	Asn	Glu	Cys	Ala	Thr				
		355					360					365							
Gln	Asn	His	Gly	Cys	Thr	Leu	Gly	Cys	Glu	Asn	Thr	Pro	Gly	Ser	Tyr				
		370				375					380								
His	Cys	Thr	Cys	Pro	Thr	Gly	Phe	Val	Leu	Leu	Pro	Asp	Gly	Lys	Gln				
385					390					395					400				
Cys	His	Glu	Leu	Val	Ser	Cys	Pro	Gly	Asn	Val	Ser	Lys	Cys	Ser	His				
				405					410					415					

Gly Cys Val Leu Thr Ser Asp Gly Pro Arg Cys Ile Cys Pro Ala Gly
 420 425 430
 Ser Val Leu Gly Arg Asp Gly Lys Thr Cys Thr Gly Cys Ser Ser Pro
 435 440 445
 Asp Asn Gly Gly Cys Ser Gln Ile Cys Leu Pro Leu Arg Pro Gly Ser
 450 455 460
 Trp Glu Cys Asp Cys Phe Pro Gly Tyr Asp Leu Gln Ser Asp Arg Lys
 465 470 475 480
 Ser Cys Ala Ala Ser Gly Pro Gln Pro Leu Leu Leu Phe Ala Asn Ser
 485 490 495
 Gln Asp Ile Arg His Met His Phe Asp Gly Thr Asp Tyr Lys Val Leu
 500 505 510
 Leu Ser Arg Gln Met Gly Met Val Phe Ala Leu Asp Tyr Asp Pro Val
 515 520 525
 Glu Ser Lys Ile Tyr Phe Ala Gln Thr Ala Leu Lys Trp Ile Glu Arg
 530 535 540
 Ala Asn Met Asp Gly Ser Gln Arg Glu Arg Leu Ile Thr Glu Gly Val
 545 550 555 560
 Asp Thr Leu Glu Gly Leu Ala Leu Asp Trp Ile Gly Arg Arg Ile Tyr
 565 570 575
 Trp Thr Asp Ser Gly Lys Ser Val Val Gly Gly Ser Asp Leu Ser Gly
 580 585 590
 Lys His His Arg Ile Ile Ile Gln Glu Arg Ile Ser Arg Pro Arg Gly
 595 600 605
 Ile Ala Val His Pro Arg Ala Arg Arg Leu Phe Trp Thr Asp Val Gly
 610 615 620
 Met Ser Pro Arg Ile Glu Ser Ala Ser Leu Gln Gly Ser Asp Arg Val
 625 630 635 640
 Leu Ile Ala Ser Ser Asn Leu Leu Glu Pro Ser Gly Ile Thr Ile Asp
 645 650 655
 Tyr Leu Thr Asp Thr Leu Tyr Trp Cys Asp Thr Lys Arg Ser Val Ile
 660 665 670
 Glu Met Ala Asn Leu Asp Gly Ser Lys Arg Arg Arg Leu Ile Gln Asn
 675 680 685
 Asp Val Gly His Pro Phe Ser Leu Ala Val Phe Glu Asp His Leu Trp
 690 695 700
 Val Ser Asp Trp Ala Ile Pro Ser Val Ile Arg Val Asn Lys Arg Thr
 705 710 715 720
 Gly Gln Asn Arg Val Arg Leu Gln Gly Ser Met Leu Lys Pro Ser Ser
 725 730 735

Leu Val Val Val His Pro Leu Ala Lys Pro Gly Ala Asp Pro Cys Leu
 740 745 750
 Tyr Arg Asn Gly Gly Cys Glu His Ile Cys Gln Glu Ser Leu Gly Thr
 755 760 765
 Ala Arg Cys Leu Cys Arg Glu Gly Phe Val Lys Ala Trp Asp Gly Lys
 770 775 780
 Met Cys Leu Pro Gln Asp Tyr Pro Ile Leu Ser Gly Glu Asn Ala Asp
 785 790 795 800
 Leu Ser Lys Glu Val Thr Ser Leu Ser Asn Ser Thr Gln Ala Glu Val
 805 810 815
 Pro Asp Asp Asp Gly Thr Glu Ser Ser Thr Leu Val Ala Glu Ile Met
 820 825 830
 Val Ser Gly Met Asn Tyr Glu Asp Asp Cys Gly Pro Gly Gly Cys Gly
 835 840 845
 Ser His Ala Arg Cys Val Ser Asp Gly Glu Thr Ala Glu Cys Gln Cys
 850 855 860
 Leu Lys Gly Phe Ala Arg Asp Gly Asn Leu Cys Ser Asp Ile Asp Glu
 865 870 875 880
 Cys Val Leu Ala Arg Ser Asp Cys Pro Ser Thr Ser Ser Arg Cys Ile
 885 890 895
 Asn Thr Glu Gly Gly Tyr Val Cys Arg Cys Ser Glu Gly Tyr Glu Gly
 900 905 910
 Asp Gly Ile Ser Cys Phe Asp Ile Asp Glu Cys Gln Arg Gly Ala His
 915 920 925
 Asn Cys Ala Glu Asn Ala Ala Cys Thr Asn Thr Glu Gly Gly Tyr Asn
 930 935 940
 Cys Thr Cys Ala Gly Arg Pro Ser Ser Pro Gly Leu Ser Cys Pro Asp
 945 950 955 960
 Ser Thr Ala Pro Ser Leu Leu Gly Glu Asp Gly His His Leu Asp Arg
 965 970 975
 Asn Ser Tyr Pro Gly Cys Pro Ser Ser Tyr Asp Gly Tyr Cys Leu Asn
 980 985 990
 Gly Gly Val Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys Asn
 995 1000 1005
 Cys Val Ile Gly Tyr Ser Gly Asp Arg Cys Gln Thr Pro Pro Ser Ser
 1010 1015 1020
 Asp Arg Gly Pro Gln Glu Ile Glu Gly Asn Ser His Leu Pro Ser Tyr
 1025 1030 1035 1040
 Arg Pro Val Gly Pro Glu Lys Leu His Ser Leu Gln Ser Ala Asn Gly
 1045 1050 1055
 Ser Cys His Glu Arg Ala Pro Asp Leu Pro Arg Gln Thr Glu Pro Val

1060

1065

1070

Gln

<210> 141

<211> 804

<212> PRT

<213> Homo sapiens

<400> 141

Met Pro Trp Gly Arg Arg Pro Thr Trp Leu Leu Leu Ala Phe Leu Leu
 1 5 10 15

Val Phe Leu Lys Ile Ser Ile Leu Ser Val Thr Ala Trp Gln Thr Gly
 20 25 30

Asn Cys Gln Pro Gly Pro Leu Glu Arg Ser Glu Arg Ser Gly Thr Cys
 35 40 45

Ala Gly Pro Ala Pro Phe Leu Val Phe Ser Gln Gly Lys Ser Ile Ser
 50 55 60

Arg Ile Asp Pro Asp Gly Thr Asn His Gln Gln Leu Val Val Asp Ala
 65 70 75 80

Gly Ile Ser Ala Asp Met Asp Ile His Tyr Lys Lys Glu Arg Leu Tyr
 85 90 95

Trp Val Asp Val Glu Arg Gln Val Leu Leu Arg Val Phe Leu Asn Gly
 100 105 110

Thr Gly Leu Glu Lys Val Cys Asn Val Glu Arg Lys Val Ser Gly Leu
 115 120 125

Ala Ile Asp Trp Ile Asp Asp Glu Val Leu Trp Val Asp Gln Gln Asn
 130 135 140

Gly Val Ile Thr Val Thr Asp Met Thr Gly Lys Asn Ser Arg Val Leu
 145 150 155 160

Leu Ser Ser Leu Lys His Pro Ser Asn Ile Ala Val Asp Pro Ile Glu
 165 170 175

Arg Leu Met Phe Trp Ser Ser Glu Val Thr Gly Ser Leu His Arg Ala
 180 185 190

His Leu Lys Gly Val Asp Val Lys Thr Leu Leu Glu Thr Gly Gly Ile
 195 200 205

Ser Val Leu Thr Leu Asp Val Leu Asp Lys Arg Leu Phe Trp Val Gln
 210 215 220

Asp Ser Gly Glu Gly Ser His Ala Tyr Ile His Ser Cys Asp Tyr Glu
 225 230 235 240

Gly Gly Ser Val Arg Leu Ile Arg His Gln Ala Arg His Ser Leu Ser
 245 250 255

Ser Met Ala Phe Phe Gly Asp Arg Ile Phe Tyr Ser Val Leu Lys Ser

260						265						270					
Lys	Ala	Ile	Trp	Ile	Ala	Asn	Lys	His	Thr	Gly	Lys	Asp	Thr	Val	Arg		
	275					280						285					
Ile	Asn	Leu	His	Pro	Ser	Phe	Val	Thr	Pro	Gly	Lys	Leu	Met	Val	Val		
	290					295					300						
His	Pro	Arg	Ala	Gln	Pro	Arg	Thr	Glu	Asp	Ala	Ala	Lys	Asp	Pro	Asp		
305					310					315					320		
Pro	Glu	Leu	Leu	Lys	Gln	Arg	Gly	Arg	Pro	Cys	Arg	Phe	Gly	Leu	Cys		
				325					330					335			
Glu	Arg	Asp	Pro	Lys	Ser	His	Ser	Ser	Ala	Cys	Ala	Glu	Gly	Tyr	Thr		
			340					345					350				
Leu	Ser	Arg	Asp	Arg	Lys	Tyr	Cys	Glu	Asp	Val	Asn	Glu	Cys	Ala	Thr		
		355					360					365					
Gln	Asn	His	Gly	Cys	Thr	Leu	Gly	Cys	Glu	Asn	Thr	Pro	Gly	Ser	Tyr		
	370					375					380						
His	Cys	Thr	Cys	Pro	Thr	Gly	Phe	Val	Leu	Leu	Pro	Asp	Gly	Lys	Gln		
385					390					395					400		
Cys	His	Glu	Leu	Val	Ser	Cys	Pro	Gly	Asn	Val	Ser	Lys	Cys	Ser	His		
				405					410					415			
Gly	Cys	Val	Leu	Thr	Ser	Asp	Gly	Pro	Arg	Cys	Ile	Cys	Pro	Ala	Gly		
			420					425					430				
Ser	Val	Leu	Gly	Arg	Asp	Gly	Lys	Thr	Cys	Thr	Gly	Cys	Ser	Ser	Pro		
		435					440					445					
Asp	Asn	Gly	Gly	Cys	Ser	Gln	Ile	Cys	Leu	Pro	Leu	Arg	Pro	Gly	Ser		
	450					455					460						
Trp	Glu	Cys	Asp	Cys	Phe	Pro	Gly	Tyr	Asp	Leu	Gln	Ser	Asp	Arg	Lys		
465					470					475					480		
Ser	Cys	Ala	Ala	Ser	Gly	Pro	Gln	Pro	Leu	Leu	Leu	Phe	Ala	Asn	Ser		
				485					490					495			
Gln	Asp	Ile	Arg	His	Met	His	Phe	Asp	Gly	Thr	Asp	Tyr	Lys	Val	Leu		
			500					505					510				
Leu	Ser	Arg	Gln	Met	Gly	Met	Val	Phe	Ala	Leu	Asp	Tyr	Asp	Pro	Val		
		515					520					525					
Glu	Ser	Lys	Ile	Tyr	Phe	Ala	Gln	Thr	Ala	Leu	Lys	Trp	Ile	Glu	Arg		
	530					535					540						
Ala	Asn	Met	Asp	Gly	Ser	Gln	Arg	Glu	Arg	Leu	Ile	Thr	Glu	Gly	Val		
545					550					555					560		
Asp	Thr	Leu	Glu	Gly	Leu	Ala	Leu	Asp	Trp	Ile	Gly	Arg	Arg	Ile	Tyr		
				565				570						575			
Trp	Thr	Asp	Ser	Gly	Lys	Ser	Val	Val	Gly	Gly	Ser	Asp	Leu	Ser	Gly		
			580					585					590				

Lys His His Arg Ile Ile Ile Gln Glu Arg Ile Ser Arg Pro Arg Gly
 595 600 605
 Ile Ala Val His Pro Arg Ala Arg Arg Leu Phe Trp Thr Asp Val Gly
 610 615 620
 Met Ser Pro Arg Ile Glu Ser Ala Ser Leu Gln Gly Ser Asp Arg Val
 625 630 635 640
 Leu Ile Ala Ser Ser Asn Leu Leu Glu Pro Ser Gly Ile Thr Ile Asp
 645 650 655
 Tyr Leu Thr Asp Thr Leu Tyr Trp Cys Asp Thr Lys Arg Ser Val Ile
 660 665 670
 Glu Met Ala Asn Leu Asp Gly Ser Lys Arg Arg Arg Leu Ile Gln Asn
 675 680 685
 Asp Val Gly His Pro Phe Ser Leu Ala Val Phe Glu Asp His Leu Trp
 690 695 700
 Val Ser Asp Trp Ala Ile Pro Ser Val Ile Arg Val Asn Lys Arg Thr
 705 710 715 720
 Gly Gln Asn Arg Val Arg Leu Gln Gly Ser Met Leu Lys Pro Ser Ser
 725 730 735
 Leu Val Val Val His Pro Leu Ala Lys Pro Gly Ala Asp Pro Cys Leu
 740 745 750
 Tyr Arg Asn Gly Gly Cys Glu His Ile Cys Gln Glu Ser Leu Gly Thr
 755 760 765
 Ala Arg Cys Leu Cys Arg Glu Gly Phe Val Lys Ala Trp Asp Gly Lys
 770 775 780
 Met Cys Leu Pro Gln Asp Tyr Pro Ile Leu Ser Gly Glu Asn Ala His
 785 790 795 800
 Asn Cys Ala Phe

<210> 142
 <211> 576
 <212> PRT
 <213> Homo sapiens

<400> 142
 Met Pro Trp Gly Arg Arg Pro Thr Trp Leu Leu Leu Ala Phe Leu Leu
 1 5 10 15
 Val Phe Leu Lys Ile Ser Ile Leu Ser Val Thr Ala Trp Gln Thr Gly
 20 25 30
 Asn Cys Gln Pro Gly Pro Leu Glu Arg Ser Glu Arg Ser Gly Thr Cys
 35 40 45
 Ala Gly Pro Ala Pro Phe Leu Val Phe Ser Gln Gly Lys Ser Ile Ser
 50 55 60

Arg Ile Trp Ala Ile Pro Ser Val Ile Arg Val Asn Lys Arg Thr Gly
 65 70 75 80
 Gln Asn Arg Val Arg Leu Gln Gly Ser Met Leu Lys Pro Ser Ser Leu
 85 90 95
 Val Val Val His Pro Leu Ala Lys Pro Gly Ala Asp Pro Cys Leu Tyr
 100 105 110
 Arg Asn Gly Gly Cys Glu His Ile Cys Gln Glu Ser Leu Gly Thr Ala
 115 120 125
 Arg Cys Leu Cys Arg Glu Gly Phe Val Lys Ala Trp Asp Gly Lys Met
 130 135 140
 Cys Leu Pro Gln Asp Tyr Pro Ile Leu Ser Gly Glu Asn Ala Asp Leu
 145 150 155 160
 Ser Lys Glu Val Thr Ser Leu Ser Asn Ser Thr Gln Ala Glu Val Pro
 165 170 175
 Asp Asp Asp Gly Thr Glu Ser Ser Thr Leu Val Ala Glu Ile Met Val
 180 185 190
 Ser Gly Met Asn Tyr Glu Asp Asp Cys Gly Pro Gly Gly Cys Gly Ser
 195 200 205
 His Ala Arg Cys Val Ser Asp Gly Glu Thr Ala Glu Cys Gln Cys Leu
 210 215 220
 Lys Gly Phe Ala Arg Asp Gly Asn Leu Cys Ser Asp Ile Asp Glu Cys
 225 230 235 240
 Val Leu Ala Arg Ser Asp Cys Pro Ser Thr Ser Ser Arg Cys Ile Asn
 245 250 255
 Thr Glu Gly Gly Tyr Val Cys Arg Cys Ser Glu Gly Tyr Glu Gly Asp
 260 265 270
 Gly Ile Ser Cys Phe Asp Ile Asp Glu Cys Gln Arg Gly Ala His Asn
 275 280 285
 Cys Ala Glu Asn Ala Ala Cys Thr Asn Thr Glu Gly Gly Tyr Asn Cys
 290 295 300
 Thr Cys Ala Gly Arg Pro Ser Ser Pro Gly Leu Ser Cys Pro Asp Ser
 305 310 315 320
 Thr Ala Pro Ser Leu Leu Gly Glu Asp Gly His His Leu Asp Arg Asn
 325 330 335
 Ser Tyr Pro Gly Cys Pro Ser Ser Tyr Asp Gly Tyr Cys Leu Asn Gly
 340 345 350
 Gly Val Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys Asn Cys
 355 360 365
 Val Ile Gly Tyr Ser Gly Asp Arg Cys Gln Thr Arg Asp Leu Arg Trp
 370 375 380

Trp Glu Leu Arg His Ala Gly Tyr Gly Gln Lys His Asp Ile Met Val
 385 390 395 400
 Val Ala Val Cys Met Val Ala Leu Val Leu Leu Leu Leu Gly Met
 405 410 415
 Trp Gly Thr Tyr Tyr Tyr Arg Thr Arg Lys Gln Leu Ser Asn Pro Pro
 420 425 430
 Lys Asn Pro Cys Asp Glu Pro Ser Gly Ser Val Ser Ser Ser Gly Pro
 435 440 445
 Asp Ser Ser Ser Gly Ala Ala Val Ala Ser Cys Pro Gln Pro Trp Phe
 450 455 460
 Val Val Leu Glu Lys His Gln Asp Pro Lys Asn Gly Ser Leu Pro Ala
 465 470 475 480
 Asp Gly Thr Asn Gly Ala Val Val Asp Ala Gly Leu Ser Pro Ser Leu
 485 490 495
 Gln Leu Gly Ser Val His Leu Thr Ser Trp Arg Gln Lys Pro His Ile
 500 505 510
 Asp Gly Met Gly Thr Gly Gln Ser Cys Trp Ile Pro Pro Ser Ser Asp
 515 520 525
 Arg Gly Pro Gln Glu Ile Glu Gly Asn Ser His Leu Pro Ser Tyr Arg
 530 535 540
 Pro Val Gly Pro Glu Lys Leu His Ser Leu Gln Ser Ala Asn Gly Ser
 545 550 555 560
 Cys His Glu Arg Ala Pro Asp Leu Pro Arg Gln Thr Glu Pro Val Gln
 565 570 575

<210> 143
 <211> 376
 <212> PRT
 <213> Homo sapiens

<400> 143
 Met Pro Trp Gly Arg Arg Pro Thr Trp Leu Leu Leu Ala Phe Leu Leu
 1 5 10 15
 Val Ser Ala Glu Cys Gln Cys Leu Lys Gly Phe Ala Arg Asp Gly Asn
 20 25 30
 Leu Cys Ser Asp Ile Asp Glu Cys Val Leu Ala Arg Ser Asp Cys Pro
 35 40 45
 Ser Thr Ser Ser Arg Cys Ile Asn Thr Glu Gly Gly Tyr Val Cys Arg
 50 55 60
 Cys Ser Glu Gly Tyr Glu Gly Asp Gly Ile Ser Cys Phe Asp Ile Asp
 65 70 75 80

Glu Cys Gln Arg Gly Ala His Asn Cys Ala Glu Asn Ala Ala Cys Thr
 85 90 95
 Asn Thr Glu Gly Gly Tyr Asn Cys Thr Cys Ala Gly Arg Pro Ser Ser
 100 105 110
 Pro Gly Leu Ser Cys Pro Asp Ser Thr Ala Pro Ser Leu Leu Gly Glu
 115 120 125
 Asp Gly His His Leu Asp Arg Asn Ser Tyr Pro Gly Cys Pro Ser Ser
 130 135 140
 Tyr Asp Gly Tyr Cys Leu Asn Gly Gly Val Cys Met His Ile Glu Ser
 145 150 155 160
 Leu Asp Ser Tyr Thr Cys Asn Cys Val Ile Gly Tyr Ser Gly Asp Arg
 165 170 175
 Cys Gln Thr Arg Asp Leu Arg Trp Trp Glu Leu Arg His Ala Gly Tyr
 180 185 190
 Gly Gln Lys His Asp Ile Met Val Val Ala Val Cys Met Val Ala Leu
 195 200 205
 Val Leu Leu Leu Leu Leu Gly Met Trp Gly Thr Tyr Tyr Tyr Arg Thr
 210 215 220
 Arg Lys Gln Leu Ser Asn Pro Pro Lys Asn Pro Cys Asp Glu Pro Ser
 225 230 235 240
 Gly Ser Val Ser Ser Ser Gly Pro Asp Ser Ser Ser Gly Ala Ala Val
 245 250 255
 Ala Ser Cys Pro Gln Pro Trp Phe Val Val Leu Glu Lys His Gln Asp
 260 265 270
 Pro Lys Asn Gly Ser Leu Pro Ala Asp Gly Thr Asn Gly Ala Val Val
 275 280 285
 Asp Ala Gly Leu Ser Pro Ser Leu Gln Leu Gly Ser Val His Leu Thr
 290 295 300
 Ser Trp Arg Gln Lys Pro His Ile Asp Gly Met Gly Thr Gly Gln Ser
 305 310 315 320
 Cys Trp Ile Pro Pro Ser Ser Asp Arg Gly Pro Gln Glu Ile Glu Gly
 325 330 335
 Asn Ser His Leu Pro Ser Tyr Arg Pro Val Gly Pro Glu Lys Leu His
 340 345 350
 Ser Leu Gln Ser Ala Asn Gly Ser Cys His Glu Arg Ala Pro Asp Leu
 355 360 365
 Pro Arg Gln Thr Glu Pro Val Gln
 370 375

<210> 144

<211> 1249

<212> PRT

<213> Homo sapiens

<400> 144

Met Gly Ala Ala Ser Gly Gln Arg Gly Arg Trp Pro Leu Ser Pro Pro
 1 5 10 15
 Leu Leu Met Leu Ser Leu Leu Val Leu Leu Leu Gln Pro Ser Pro Ala
 20 25 30
 Pro Ala Leu Asp Pro Gly Leu Gln Pro Gly Asn Phe Ser Pro Asp Glu
 35 40 45
 Ala Gly Ala Gln Leu Phe Ala Glu Ser Tyr Asn Ser Ser Ala Glu Val
 50 55 60
 Val Met Phe Gln Ser Thr Val Ala Ser Trp Ala His Asp Thr Asn Ile
 65 70 75 80
 Thr Glu Glu Asn Ala Arg Arg Gln Glu Glu Ala Ala Leu Val Ser Gln
 85 90 95
 Glu Phe Ala Glu Val Trp Gly Lys Lys Ala Lys Glu Leu Tyr Glu Ser
 100 105 110
 Ile Trp Gln Asn Phe Thr Asp Ser Lys Leu Arg Arg Ile Ile Gly Ser
 115 120 125
 Ile Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Gln Arg Gln Gln
 130 135 140
 Tyr Asn Ser Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr Gly Lys
 145 150 155 160
 Val Cys Phe Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Glu
 165 170 175
 Leu Thr Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Lys Leu Leu Phe
 180 185 190
 Ala Trp Glu Gly Trp His Asp Ala Val Gly Ile Pro Leu Lys Pro Leu
 195 200 205
 Tyr Gln Asp Phe Thr Ala Ile Ser Asn Glu Ala Tyr Arg Gln Asp Asp
 210 215 220
 Phe Ser Asp Thr Gly Ala Phe Trp Arg Ser Trp Tyr Glu Ser Pro Ser
 225 230 235 240
 Phe Glu Glu Ser Leu Glu His Ile Tyr His Gln Leu Glu Pro Leu Tyr
 245 250 255
 Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg Arg Tyr Gly
 260 265 270
 Asp Lys Tyr Val Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly
 275 280 285
 Asp Met Trp Ala Gln Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro
 290 295 300
 Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln Lys

305		310		315		320
Gly Trp Asn Ala Thr	His Met Phe Arg Val Ser Glu Glu Phe Phe Thr					
	325		330		335	
Ser Leu Gly Leu Ser Pro Met Pro Pro Glu Phe Trp Ala Glu Ser Met						
	340		345		350	
Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser Ala						
	355		360		365	
Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg						
	370		375		380	
Val Thr Met Glu Gln Leu Ala Thr Val His His Glu Met Gly His Val						
	385		390		395	400
Gln Tyr Tyr Leu Gln Tyr Lys Asp Leu His Val Ser Leu Arg Arg Gly						
	405		410		415	
Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser						
	420		425		430	
Val Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp His Val						
	435		440		445	
Thr Asn Asp Ile Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu						
	450		455		460	
Glu Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg						
	465		470		475	480
Trp Gly Val Phe Ser Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp						
	485		490		495	
Trp Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Ala						
	500		505		510	
Arg Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro Asn						
	515		520		525	
Val Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln						
	530		535		540	
Phe His Gln Ala Leu Cys Lys Glu Ala Gly His Gln Gly Pro Leu His						
	545		550		555	560
Gln Cys Asp Ile Tyr Gln Ser Xaa Gln Ala Gly Ala Lys Leu Lys Gln						
	565		570		575	
Val Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys Asp						
	580		585		590	
Leu Val Gly Ser Asp Ala Leu Asp Ala Lys Ala Leu Leu Glu Tyr Phe						
	595		600		605	
Gln Pro Val Ser Gln Trp Leu Glu Glu Gln Asn Gln Arg Asn Gly Glu						
	610		615		620	
Val Leu Gly Trp Pro Glu Asn Gln Trp Arg Pro Pro Leu Pro Asp Asn						
	625		630		635	640

Tyr Pro Glu Gly Ile Asp Leu Glu Thr Asp Glu Ala Lys Ala Asp Arg
 645 650 655
 Phe Val Glu Glu Tyr Asp Arg Thr Ala Gln Val Leu Leu Asn Glu Tyr
 660 665 670
 Ala Glu Ala Asn Trp Gln Tyr Asn Thr Asn Ile Thr Ile Glu Gly Ser
 675 680 685
 Lys Ile Leu Leu Glu Lys Ser Thr Glu Val Ser Asn His Thr Leu Lys
 690 695 700
 Tyr Gly Thr Arg Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn Ser
 705 710 715 720
 Ser Ile Lys Arg Ile Ile Lys Lys Leu Gln Asn Leu Asp Arg Ala Val
 725 730 735
 Leu Pro Pro Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met
 740 745 750
 Glu Thr Thr Tyr Ser Leu Ser Asn Ile Cys Tyr Thr Asn Gly Thr Cys
 755 760 765
 Met Pro Leu Glu Pro Asp Leu Thr Asn Met Met Ala Thr Ser Arg Lys
 770 775 780
 Tyr Glu Glu Leu Leu Trp Ala Trp Lys Ser Trp Arg Asp Lys Val Gly
 785 790 795 800
 Arg Ala Ile Leu Pro Phe Phe Pro Lys Tyr Val Glu Phe Ser Asn Lys
 805 810 815
 Ile Ala Lys Leu Asn Gly Tyr Thr Asp Ala Gly Asp Ser Trp Arg Ser
 820 825 830
 Leu Tyr Glu Ser Asp Asn Leu Glu Gln Asp Leu Glu Lys Leu Tyr Gln
 835 840 845
 Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ser
 850 855 860
 Leu His Arg His Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly Pro Ile
 865 870 875 880
 Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile
 885 890 895
 Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Pro Asn Ile Asp Ala Thr
 900 905 910
 Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys Glu
 915 920 925
 Ala Asp Asn Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu
 930 935 940
 Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val
 945 950 955 960

Val Cys His Pro Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg
 965 970 975
 Ile Lys Gln Cys Thr Ser Val Asn Met Glu Asp Leu Val Ile Ala His
 980 985 990
 His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro
 995 1000 1005
 Val Thr Phe Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly
 1010 1015 1020
 Asp Ile Met Ala Leu Ser Val Ser Thr Pro Lys His Leu Tyr Ser Leu
 1025 1030 1035 1040
 Asn Leu Leu Ser Thr Glu Gly Ser Gly Tyr Glu Tyr Asp Ile Asn Phe
 1045 1050 1055
 Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr
 1060 1065 1070
 Leu Ile Asp Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys
 1075 1080 1085
 Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly
 1090 1095 1100
 Leu Cys Pro Pro Val Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ser
 1105 1110 1115 1120
 Lys Phe His Val Pro Ala Asn Val Pro Tyr Val Arg Tyr Phe Val Ser
 1125 1130 1135
 Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Arg Ala Ala Gly
 1140 1145 1150
 His Thr Gly Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala
 1155 1160 1165
 Gly Lys Leu Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp
 1170 1175 1180
 Pro Glu Ala Met Lys Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser
 1185 1190 1195 1200
 Ala Met Met Asn Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr Glu
 1205 1210 1215
 Asn Arg Arg His Gly Glu Thr Leu Gly Trp Pro Glu Tyr Asn Trp Ala
 1220 1225 1230
 Pro Asn Thr Gly Thr Thr Pro Thr Leu Pro Pro Ala Pro Gly Pro Ser
 1235 1240 1245
 Ser

<210> 145

<211> 382

<212> PRT

<213> Homo sapiens

<400> 145

Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His
 1 5 10 15

Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys
 20 25 30

Met Pro Met Glu Arg Ala Leu Gly Glu Val Tyr Val Asp Asn Ser Lys
 35 40 45

Pro Thr Val Phe Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
 50 55 60

Ala Ala Ala Ala Ala Ala Ala Ala Ser Ala Pro Val Tyr Gly Gln Ser
 65 70 75 80

Gly Ile Ala Tyr Gly Pro Gly Ser Glu Ala Ala Ala Phe Ser Ala Asn
 85 90 95

Ser Leu Gly Ala Phe Pro Gln Leu Asn Ser Val Ser Pro Ser Pro Leu
 100 105 110

Met Leu Leu His Pro Pro Pro Gln Leu Ser Pro Phe Leu His Pro His
 115 120 125

Gly Gln Gln Val Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Ala Tyr Ala
 130 135 140

Val Arg Asp Thr Gly Pro Pro Ala Phe Tyr Arg Ser Asn Ser Asp Asn
 145 150 155 160

Arg Arg Gln Asn Gly Arg Glu Arg Leu Ser Ser Ser Asn Glu Lys Gly
 165 170 175

Asn Met Ile Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys
 180 185 190

Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly
 195 200 205

Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met
 210 215 220

Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser
 225 230 235 240

Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys
 245 250 255

Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys
 260 265 270

Arg Gln Arg Asp Asp Leu Glu Gly Arg Asn Glu Met Gly Ala Ser Gly
 275 280 285

Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Val Ile Lys His
 290 295 300

Thr Lys Lys Asn Ser Pro Ala Leu Ser Leu Thr Ala Asp Gln Met Val

305 310 315 320
 Ser Ala Leu Leu Asp Ala Glu Pro Pro Met Ile Tyr Ser Glu Tyr Asp
 325 330 335
 Pro Ser Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn
 340 345 350
 Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val
 355 360 365
 Pro Gly Lys Asp Ala Lys Leu Asn Phe Tyr Val Lys Ser Glu
 370 375 380

<210> 146
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 146
 Met Val Pro Gln Ala His Gly Leu Leu Leu Leu Cys Phe Leu Leu Gln
 1 5 10 15
 Leu Gln Gly Pro Leu Gly Thr Ala Val Phe Ile Thr Gln Glu Glu Ala
 20 25 30
 His Gly Val Leu His Arg Gln Arg Arg Ala Asn Ser Leu Leu Glu Glu
 35 40 45
 Leu Trp Pro Gly Ser Leu Glu Arg Glu Cys Asn Glu Glu Gln Cys Ser
 50 55 60
 Phe Glu Glu Ala Arg Glu Ile Phe Lys Ser Pro Glu Arg Thr Lys Gln
 65 70 75 80
 Phe Trp Ile Val Tyr Ser Asp Gly Asp Gln Cys Ala Ser Asn Pro Cys
 85 90 95
 Gln Asn Gly Gly Thr Cys Gln Asp His Leu Lys Ser Tyr Val Cys Phe
 100 105 110
 Cys Leu Leu Asp Phe Glu Gly Ala Val Leu Leu Asp Ala Arg Trp Ile
 115 120 125
 Val Thr Ala Ala His Cys Phe Asp Asn Ile Arg Tyr Trp Gly Asn Ile
 130 135 140
 Thr Val Val Met Gly Glu His Asp Phe Ser Glu Lys Asp Gly Asp Glu
 145 150 155 160
 Gln Val Arg Arg Val Thr Gln Val Ile Met Pro Asp Lys Tyr Ile Arg
 165 170 175
 Gly Lys Ile Asn His Asp Ile Ala Leu Leu Arg Leu His Arg Pro Val
 180 185 190
 Thr Phe Thr Asp Tyr Val Val Pro Leu Cys Leu Pro Glu Lys Ser Phe
 195 200 205
 Ser Glu Asn Thr Leu Ala Arg Ile Arg Phe Ser Arg Val Ser Gly Trp

210 215 220
 Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Ser Ile
 225 230 235 240
 Glu Val Pro Arg Leu Met Thr Gln Asp Cys Leu Glu His Ala Lys His
 245 250 255
 Ser Ser Asn Thr Pro Lys Ile Thr Glu Asn Met Phe Cys Ala Gly Tyr
 260 265 270
 Met Asp Gly Thr Lys Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro His
 275 280 285
 Ala Thr His Tyr His Gly Thr Trp Tyr Leu Thr Gly Val Val Ser Trp
 290 295 300
 Gly Glu Gly Cys Ala Ala Ile Gly His Ile Gly Val Tyr Thr Arg Val
 305 310 315 320
 Ser Gln Tyr Ile Asp Trp Leu Val Arg His Met Asp Ser Lys Leu Gln
 325 330 335
 Val Gly Val Phe Arg Leu Pro Leu Leu
 340 345

<210> 147
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 147
 Met Gly Phe Leu Lys Phe Ser Pro Phe Leu Val Val Ser Ile Leu Leu
 1 5 10 15
 Leu Ala Leu Val Gln Asp Tyr Met Gln Met Lys Ala Arg Glu Leu Glu
 20 25 30
 Gln Glu Glu Glu Gln Glu Ala Glu Gly Ser Ser Leu Asp Ser Pro Arg
 35 40 45
 Ser Lys Arg Cys Gly Asn Leu Ser Thr Cys Met Leu Gly Thr Tyr Thr
 50 55 60
 Gln Asp Leu Asn Lys Phe His Thr Phe Pro Gln Thr Ser Ile Gly Val
 65 70 75 80
 Glu Ala Pro Gly Lys Lys Arg Asp Val Ala Lys Asp Leu Glu Thr Asn
 85 90 95
 His Gln Ser His Phe Gly Asn
 100

<210> 148
 <211> 525
 <212> PRT
 <213> Homo sapiens

<400> 148

Met Ala Thr Leu Leu Arg Ser Lys Leu Thr Asn Val Ala Thr Ser Val
 1 5 10 15
 Ser Asn Lys Ser Gln Ala Lys Val Ser Gly Met Phe Ala Arg Met Gly
 20 25 30
 Phe Gln Ala Ala Thr Asp Glu Glu Ala Val Gly Phe Ala His Cys Asp
 35 40 45
 Asp Leu Asp Phe Glu His Arg Gln Gly Leu Gln Met Asp Ile Leu Lys
 50 55 60
 Ser Glu Gly Glu Pro Cys Gly Asp Glu Gly Ala Glu Ala Pro Val Glu
 65 70 75 80
 Gly Asp Ile His Tyr Gln Arg Gly Gly Ala Pro Leu Pro Pro Ser Gly
 85 90 95
 Ser Lys Asp Gln Ala Val Gly Ala Gly Gly Glu Phe Gly Gly His Asp
 100 105 110
 Lys Pro Lys Ile Thr Ala Trp Glu Ala Gly Trp Asn Val Thr Asn Ala
 115 120 125
 Ile Gln Gly Met Phe Val Leu Gly Leu Pro Tyr Ala Ile Leu His Gly
 130 135 140
 Gly Tyr Leu Gly Leu Phe Leu Ile Ile Phe Ala Ala Val Val Cys Cys
 145 150 155 160
 Tyr Thr Gly Lys Ile Leu Ile Ala Cys Leu Tyr Glu Glu Asn Glu Asp
 165 170 175
 Gly Glu Val Val Arg Val Arg Asp Ser Tyr Val Ala Ile Ala Asn Ala
 180 185 190
 Cys Cys Ala Pro Arg Phe Pro Thr Leu Gly Gly Arg Val Val Asn Val
 195 200 205
 Ala Gln Ile Ile Glu Leu Val Met Thr Cys Ile Leu Tyr Val Val Val
 210 215 220
 Ser Gly Asn Leu Met Tyr Asn Ser Phe Pro Gly Leu Pro Val Ser Gln
 225 230 235 240
 Lys Ser Trp Ser Ile Ile Ala Thr Ala Val Leu Leu Pro Cys Ala Phe
 245 250 255
 Leu Lys Asn Leu Lys Ala Val Ser Lys Phe Ser Leu Leu Cys Thr Leu
 260 265 270
 Ala His Phe Val Ile Asn Ile Leu Val Ile Ala Tyr Cys Leu Ser Arg
 275 280 285
 Ala Arg Asp Trp Ala Trp Glu Lys Val Lys Phe Tyr Ile Asp Val Lys
 290 295 300
 Lys Phe Pro Ile Ser Ile Gly Ile Ile Val Phe Ser Tyr Thr Ser Gln
 305 310 315 320
 Ile Phe Leu Pro Ser Leu Glu Gly Asn Met Gln Gln Pro Ser Glu Phe

	325		330		335
His Cys Met	Met Asn Trp Thr	His Ile Ala Ala Cys Val	Leu Lys Gly		
	340	345	350		
Leu Phe Ala	Leu Val Ala Tyr	Leu Thr Trp Ala Asp	Glu Thr Lys Glu		
	355	360	365		
Val Ile Thr	Asp Asn Leu Pro	Gly Ser Ile Arg Ala	Val Val Asn Leu		
	370	375	380		
Phe Leu Val	Ala Lys Ala Leu Leu	Ser Tyr Pro Leu Pro	Phe Phe Ala		
	385	390	395	400	
Ala Val Glu	Val Leu Glu Lys Ser	Leu Phe Gln Glu Gly	Ser Arg Ala		
	405	410	415		
Phe Phe Pro	Ala Cys Tyr Gly	Gly Asp Gly Arg Leu	Lys Ser Trp Glu		
	420	425	430		
Leu Thr Leu	Arg Cys Ala Leu	Val Val Phe Thr	Leu Leu Met Ala Ile		
	435	440	445		
Tyr Val Pro	His Phe Ala Leu	Leu Met Gly Leu Thr	Gly Ser Leu Thr		
	450	455	460		
Gly Ala Gly	Leu Cys Phe Leu Leu	Pro Ser Leu Phe His	Leu Arg Leu		
	465	470	475	480	
Leu Trp Arg	Lys Leu Leu Trp	His Gln Val Phe Phe	Asp Val Ala Ile		
	485	490	495		
Phe Val Ile	Gly Gly Ile Cys Ser	Val Ser Gly Phe Val	His Ser Leu		
	500	505	510		
Glu Gly Leu	Ile Glu Ala Tyr Arg	Thr Asn Ala Glu Asp			
	515	520	525		

<210> 149

<211> 400

<212> PRT

<213> Homo sapiens

<400> 149

Met Asp Val	Leu Ala Glu Ala	Asn Gly Thr Phe	Ala Leu Asn Leu Leu
1	5	10	15
Lys Thr Leu	Gly Lys Asp Asn Ser	Lys Asn Val Phe Phe	Ser Pro Met
	20	25	30
Ser Met Ser	Cys Ala Leu Ala	Met Val Tyr Met	Gly Ala Lys Gly Asn
	35	40	45
Thr Ala Ala	Gln Met Ala Gln	Ile Leu Ser Phe	Asn Lys Ser Gly Gly
	50	55	60
Gly Gly Asp	Ile His Gln Gly	Phe Gln Ser Leu	Leu Thr Glu Val Asn
	65	70	75
Lys Thr Gly	Thr Gln Tyr Leu	Leu Arg Val Ala	Asn Arg Leu Phe Gly

85										90					95				
Glu	Lys	Ser	Cys	Asp	Phe	Leu	Ser	Ser	Phe	Arg	Asp	Ser	Cys	Gln	Lys				
			100					105					110						
Phe	Tyr	Gln	Ala	Glu	Met	Glu	Glu	Leu	Asp	Phe	Ile	Ser	Ala	Val	Glu				
		115					120					125							
Lys	Ser	Arg	Lys	His	Ile	Asn	Thr	Trp	Val	Ala	Glu	Lys	Thr	Glu	Gly				
	130					135					140								
Lys	Ile	Ala	Glu	Leu	Leu	Ser	Pro	Gly	Ser	Val	Asp	Pro	Leu	Thr	Arg				
145					150					155					160				
Leu	Val	Leu	Val	Asn	Ala	Val	Tyr	Phe	Arg	Gly	Asn	Trp	Asp	Glu	Gln				
				165					170					175					
Phe	Asp	Lys	Glu	Asn	Thr	Glu	Glu	Arg	Leu	Phe	Lys	Val	Ser	Lys	Asn				
			180					185					190						
Glu	Glu	Lys	Pro	Val	Gln	Met	Met	Phe	Lys	Gln	Ser	Thr	Phe	Lys	Lys				
		195					200					205							
Thr	Tyr	Ile	Gly	Glu	Ile	Phe	Thr	Gln	Ile	Leu	Val	Leu	Pro	Tyr	Val				
	210					215					220								
Gly	Lys	Glu	Leu	Asn	Met	Ile	Ile	Met	Leu	Pro	Asp	Glu	Thr	Thr	Asp				
225				230					235						240				
Leu	Arg	Thr	Val	Glu	Lys	Glu	Leu	Thr	Tyr	Glu	Lys	Phe	Val	Glu	Trp				
			245						250					255					
Thr	Arg	Leu	Asp	Met	Met	Asp	Glu	Glu	Glu	Val	Glu	Val	Ser	Leu	Pro				
		260					265						270						
Arg	Phe	Lys	Leu	Glu	Glu	Ser	Tyr	Asp	Met	Glu	Ser	Val	Leu	Arg	Asn				
		275					280					285							
Leu	Gly	Met	Thr	Asp	Ala	Phe	Glu	Leu	Gly	Lys	Ala	Asp	Phe	Ser	Gly				
	290					295					300								
Met	Ser	Gln	Thr	Asp	Leu	Ser	Leu	Ser	Lys	Val	Val	His	Lys	Ser	Phe				
305					310					315				320					
Val	Glu	Val	Asn	Glu	Glu	Gly	Thr	Glu	Ala	Ala	Ala	Ala	Thr	Ala	Ala				
			325						330					335					
Ile	Met	Met	Met	Arg	Cys	Ala	Arg	Phe	Val	Pro	Arg	Phe	Cys	Ala	Asp				
			340					345					350						
His	Pro	Phe	Leu	Phe	Phe	Ile	Gln	His	Ser	Lys	Thr	Asn	Gly	Ile	Leu				
		355					360					365							
Phe	Cys	Gly	Arg	Gln	Leu	Met	Asn	Phe	Ser	Pro	Asp	Ser	Ser	Ala	Gly				
	370					375					380								
Cys	Cys	Asn	Val	Xaa	Leu	Phe	Pro	Ser	Pro	Trp	Gly	Gly	Gly	Gly	Gly				
385					390					395					400				

<210> 150
 <211> 372
 <212> PRT
 <213> Homo sapiens

<400> 150

Met	Asp	Val	Leu	Ala	Glu	Ala	Asn	Gly	Thr	Phe	Ala	Leu	Asn	Leu	Leu
1				5					10					15	
Lys	Thr	Leu	Gly	Lys	Asp	Asn	Ser	Lys	Asn	Val	Phe	Phe	Ser	Pro	Met
			20					25					30		
Ser	Met	Ser	Cys	Ala	Leu	Ala	Met	Val	Tyr	Met	Gly	Ala	Lys	Gly	Asn
		35					40					45			
Thr	Ala	Ala	Gln	Met	Ala	Gln	Ile	Leu	Ser	Phe	Asn	Lys	Ser	Gly	Gly
	50					55					60				
Gly	Gly	Asp	Ile	His	Gln	Gly	Phe	Gln	Ser	Leu	Leu	Thr	Glu	Val	Asn
65					70					75					80
Lys	Thr	Gly	Thr	Gln	Tyr	Leu	Leu	Arg	Val	Ala	Asn	Arg	Leu	Phe	Gly
				85					90					95	
Glu	Lys	Ser	Cys	Asp	Phe	Leu	Ser	Ser	Phe	Arg	Asp	Ser	Cys	Gln	Lys
			100					105					110		
Phe	Tyr	Gln	Ala	Glu	Met	Glu	Glu	Leu	Asp	Phe	Ile	Ser	Ala	Val	Glu
	115						120					125			
Lys	Ser	Arg	Lys	His	Ile	Asn	Thr	Trp	Val	Ala	Glu	Lys	Thr	Glu	Gly
	130					135					140				
Lys	Ile	Ala	Glu	Leu	Leu	Ser	Pro	Gly	Ser	Val	Asp	Pro	Leu	Thr	Arg
145					150					155					160
Leu	Val	Leu	Val	Asn	Ala	Val	Tyr	Phe	Arg	Gly	Asn	Trp	Asp	Glu	Gln
				165					170					175	
Phe	Asp	Lys	Glu	Asn	Thr	Glu	Glu	Arg	Leu	Phe	Lys	Val	Ser	Lys	Asn
			180					185					190		
Glu	Glu	Lys	Pro	Val	Gln	Met	Met	Phe	Lys	Gln	Ser	Thr	Phe	Lys	Lys
		195					200					205			
Thr	Tyr	Ile	Gly	Glu	Ile	Phe	Thr	Gln	Ile	Leu	Val	Leu	Pro	Tyr	Val
	210					215					220				
Gly	Lys	Glu	Leu	Asn	Met	Ile	Ile	Met	Leu	Pro	Asp	Glu	Thr	Thr	Asp
225					230					235					240
Leu	Arg	Thr	Val	Glu	Lys	Glu	Leu	Thr	Tyr	Glu	Lys	Phe	Val	Glu	Trp
				245					250					255	
Thr	Arg	Leu	Asp	Met	Met	Asp	Glu	Glu	Glu	Val	Glu	Val	Ser	Leu	Pro
			260					265					270		
Arg	Phe	Lys	Leu	Glu	Glu	Ser	Tyr	Asp	Met	Glu	Ser	Val	Leu	Arg	Asn
		275					280					285			

Leu Gly Met Thr Asp Ala Phe Glu Leu Gly Lys Ala Asp Phe Ser Gly
 290 295 300

Met Ser Gln Thr Asp Leu Ser Leu Ser Lys Val Val His Lys Ser Phe
 305 310 315 320

Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Thr Ala Ala
 325 330 335

Ile Met Met Met Arg Cys Ala Arg Phe Val Pro Arg Phe Cys Ala Asp
 340 345 350

His Pro Phe Leu Phe Phe Ile Gln Gln Arg Ile Pro Leu Val Leu Leu
 355 360 365

Cys Trp Ser Thr
 370

<210> 151

<211> 560

<212> PRT

<213> Homo sapiens

<400> 151

Met Phe Pro Asp Leu Val Gln Leu Ile Cys Ala Tyr Cys His Thr Arg
 1 5 10 15

Asp Ile Leu Leu Leu Pro Leu Gln Leu Pro Arg Ala Ile His His Ala
 20 25 30

Ala Thr His Lys Glu Leu Glu Ala Ile Ser His Leu Gly Ile Glu Phe
 35 40 45

Trp Ser Ser Ser Leu Asn Ile Lys Ala Gln Arg Gly Pro Ala Gly Gly
 50 55 60

Pro Val Leu Pro Gln Leu Lys Ala Arg Ser Pro Gln Glu Leu Asp Gln
 65 70 75 80

Gly Thr Gly Ala Ala Leu Cys Phe Phe Asn Pro Leu Phe Pro Gly Asp
 85 90 95

Leu Gly Pro Thr Lys Arg Glu Lys Phe Lys Arg Ser Phe Lys Val Arg
 100 105 110

Val Ser Thr Glu Thr Ser Ser Pro Leu Ser Pro Pro Ala Val Pro Pro
 115 120 125

Pro Pro Val Pro Val Leu Pro Gly Ala Val Pro Ser Gln Thr Glu Arg
 130 135 140

Leu Pro Pro Cys Gln Leu Leu Arg Arg Glu Ser Ser Val Gly Tyr Arg
 145 150 155 160

Val Pro Ala Gly Ser Gly Pro Ser Leu Pro Pro Met Pro Ser Leu Gln
 165 170 175

Glu Val Asp Cys Gly Ser Pro Ser Ser Ser Glu Glu Glu Gly Val Pro
 180 185 190

Gly Ser Arg Gly Ser Pro Ala Thr Ser Pro His Leu Gly Arg Arg Arg
 195 200 205
 Pro Leu Leu Arg Ser Met Ser Ala Ala Phe Cys Ser Leu Leu Ala Pro
 210 215 220
 Glu Arg Gln Val Gly Arg Ala Ala Ala Ala Leu Met Gln Asp Arg His
 225 230 235 240
 Thr Ala Ala Gly Gln Leu Val Gln Asp Leu Leu Thr Gln Val Arg Asp
 245 250 255
 Gly Gln Arg Pro Gln Glu Leu Glu Gly Ile Arg Gln Ala Leu Ser Arg
 260 265 270
 Ala Arg Ala Met Leu Ser Ala Glu Leu Gly Pro Glu Lys Leu Val Ser
 275 280 285
 Pro Lys Arg Leu Glu His Val Leu Glu Lys Ser Leu His Cys Ser Val
 290 295 300
 Leu Lys Pro Leu Arg Pro Ile Leu Ala Ala Arg Leu Arg Arg Arg Leu
 305 310 315 320
 Ala Ala Asp Gly Ser Leu Gly Arg Leu Ala Glu Gly Leu Arg Leu Ala
 325 330 335
 Arg Ala Gln Gly Pro Gly Ala Phe Gly Ser His Leu Ser Leu Pro Ser
 340 345 350
 Pro Val Glu Leu Glu Gln Val Arg Gln Lys Leu Leu Gln Leu Val Arg
 355 360 365
 Thr Tyr Ser Pro Ser Ala Gln Val Lys Arg Leu Leu Gln Ala Cys Lys
 370 375 380
 Leu Leu Tyr Met Ala Leu Arg Thr Gln Glu Gly Glu Gly Ser Gly Ala
 385 390 395 400
 Asp Gly Phe Leu Pro Leu Leu Ser Leu Val Leu Ala His Cys Asp Leu
 405 410 415
 Pro Glu Leu Leu Leu Glu Ala Glu Tyr Met Ser Glu Leu Leu Glu Pro
 420 425 430
 Ser Leu Leu Thr Gly Glu Gly Gly Tyr Tyr Leu Thr Ser Leu Ser Ala
 435 440 445
 Ser Leu Ala Leu Leu Ser Gly Leu Gly Gln Ala His Thr Leu Pro Leu
 450 455 460
 Ser Pro Val Gln Glu Leu Arg Arg Ser Leu Ser Leu Trp Glu Gln Arg
 465 470 475 480
 Arg Leu Pro Ala Thr His Cys Phe Gln Val Thr Gly Pro Pro Pro Cys
 485 490 495
 Pro Gln Ser Gln Thr Pro Ser Pro Pro Xaa Thr Phe Leu Ser Leu Val
 500 505 510

Lys	Ser	Pro	Asp	Ser	Val	Asp	Arg	Ser	Trp	Val	Leu	Ile	Leu	Ala	Leu
		515					520					525			
His	Trp	Val	Val	Gly	Thr	Trp	Ala	Ser	Tyr	Leu	Thr	Thr	Ser	Cys	Leu
	530					535					540				
Ser	Phe	Leu	Ile	Ser	Lys	Met	Gly	Val	Ile	Gly	Pro	Thr	Ser	Trp	Gly
545					550					555					560

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<210> 152
<211> 437
<212> PRT
<213> Homo sapiens
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<400> 152																
Met	Leu	Ile	Ala	Ala	Gly	Pro	Ala	Arg	Thr	Gly	Val	Gly	Pro	Ala	Arg	
1				5					10					15		
Ile	Lys	Gly	Ala	Gln	Ala	Gly	Trp	Ala	Phe	His	Arg	Pro	Ser	Ala	Leu	
			20					25					30			
Cys	Ser	Arg	Gly	Ala	Gly	Gln	Ala	Xaa	Ala	Ser	Glu	Leu	Ala	Ser	Arg	
		35					40					45				
His	Arg	Gly	Gly	Ala	Ala	Ala	Val	Arg	Thr	Arg	Gln	Ala	Asn	Pro	Thr	
	50					55					60					
Gln	Lys	Ser	Pro	Pro	Pro	Asp	Ser	Gln	Val	Ala	Ala	Ala	Ser	Leu	Ala	
65					70					75					80	
His	Ala	Glu	Ser	Gly	Gly	Ala	Gly	Ser	Pro	Leu	Arg	Pro	Ala	Ser	Ala	
				85					90					95		
Leu	Ser	Ser	Ser	Pro	Phe	Pro	Phe	Phe	Ser	Leu	Ser	Ser	Pro	Leu	Ser	
			100					105					110			
Leu	Pro	Ala	Phe	Ala	Gln	Pro	Arg	Ala	Met	Ser	Asp	Ala	Ser	Leu	Arg	
		115					120					125				
Ser	Thr	Ser	Thr	Met	Glu	Arg	Leu	Val	Ala	Arg	Gly	Thr	Phe	Pro	Val	
	130					135					140					
Leu	Val	Arg	Thr	Ser	Ala	Cys	Arg	Ser	Leu	Phe	Gly	Pro	Val	Asp	His	
145					150					155					160	
Glu	Glu	Leu	Ser	Arg	Glu	Leu	Gln	Ala	Arg	Leu	Ala	Glu	Leu	Asn	Ala	
				165					170					175		
Glu	Asp	Gln	Asn	Arg	Trp	Asp	Tyr	Asp	Phe	Gln	Gln	Asp	Met	Pro	Leu	
			180					185					190			
Arg	Gly	Pro	Gly	Arg	Leu	Gln	Trp	Thr	Glu	Val	Asp	Ser	Asp	Ser	Val	
		195					200					205				
Pro	Ala	Phe	Tyr	Arg	Glu	Thr	Val	Gln	Val	Gly	Arg	Cys	Arg	Leu	Leu	
	210					215				220						

Leu Ala Pro Arg Pro Val Ala Val Ala Val Ala Val Ser Pro Pro Leu
 225 230 235 240
 Glu Pro Ala Ala Glu Ser Leu Asp Gly Leu Glu Glu Ala Pro Glu Gln
 245 250 255
 Leu Pro Ser Val Pro Val Pro Ala Pro Ala Ser Thr Pro Pro Pro Val
 260 265 270
 Pro Val Leu Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Val Ala Ala
 275 280 285
 Pro Val Ala Ala Pro Val Ala Val Pro Val Leu Ala Pro Ala Pro Ala
 290 295 300
 Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Val Ala Ala Pro Ala
 305 310 315 320
 Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala
 325 330 335
 Pro Asp Ala Ala Pro Gln Glu Ser Ala Glu Gln Gly Ala Asn Gln Gly
 340 345 350
 Gln Arg Gly Gln Glu Pro Leu Ala Asp Gln Leu His Ser Gly Ile Ser
 355 360 365
 Gly Arg Pro Ala Ala Gly Thr Ala Ala Ala Ser Ala Asn Gly Ala Ala
 370 375 380
 Ile Lys Lys Leu Ser Gly Pro Leu Ile Ser Asp Phe Phe Ala Lys Arg
 385 390 395 400
 Lys Arg Ser Ala Pro Glu Lys Ser Ser Gly Asp Val Pro Ala Pro Cys
 405 410 415
 Pro Ser Pro Ser Ala Ala Pro Gly Val Gly Ser Val Glu Gln Thr Pro
 420 425 430
 Arg Lys Arg Leu Arg
 435

<210> 153
 <211> 172
 <212> PRT
 <213> Homo sapiens

<400> 153
 Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
 1 5 10 15
 Ala Ser Ala Ala Ala Arg Gly Leu Val Glu Lys Val Arg Gln Leu Leu
 20 25 30
 Glu Ala Gly Ala Asp Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
 35 40 45
 Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
 50 55 60

Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
 65 70 75 80
 Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
 85 90 95
 Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
 100 105 110
 Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
 115 120 125
 Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
 130 135 140
 Ile Asp Ala Ala Glu Gly Pro Ser Val Thr Ala Ser Ile Gln Val Pro
 145 150 155 160
 Gly Gly Glu Glu Gly Asp Phe Gly Ser Ser Tyr Ser
 165 170

<210> 154
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 154

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu
 1 5 10 15
 Gly Leu Ala Ser Ala Ala Ala Arg Gly Leu Val Glu Lys Val Arg Gln
 20 25 30
 Leu Leu Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg
 35 40 45
 Arg Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu
 50 55 60
 Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu
 65 70 75 80
 Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu
 85 90 95
 Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp
 100 105 110
 Gly Arg Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val
 115 120 125
 Ala Arg Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His
 130 135 140
 Ala Arg Ile Asp Ala Ala Glu Gly Pro Ser Val Thr Ala Ser Ile Gln
 145 150 155 160
 Val Pro Gly Gly Glu Glu Gly Asp Phe Gly Ser Ser Tyr Ser
 165 170

<210> 155
 <211> 349
 <212> PRT
 <213> Homo sapiens

<400> 155

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Met Lys His Ser Leu Asn Ala Leu Leu Ile Phe Leu Ile Ile Thr Ser
 1              5              10              15

Ala Trp Gly Gly Ser Lys Gly Pro Leu Asp Gln Leu Glu Lys Gly Gly
      20              25              30

Glu Thr Ala Gln Ser Ala Asp Pro Gln Trp Glu Gln Leu Asn Asn Lys
      35              40              45

Asn Leu Ser Met Pro Leu Leu Pro Ala Asp Phe His Lys Glu Asn Thr
      50              55              60

Val Thr Asn Asp Trp Ile Pro Glu Gly Glu Glu Asp Asp Asp Tyr Leu
      65              70              75              80

Asp Leu Glu Lys Ile Phe Ser Glu Asp Asp Asp Tyr Ile Asp Ile Val
      85              90              95

Asp Ser Leu Ser Val Ser Pro Thr Asp Ser Asp Val Ser Ala Gly Asn
      100             105             110

Ile Leu Gln Leu Phe His Gly Lys Ser Arg Ile Gln Arg Leu Asn Ile
      115             120             125

Leu Asn Ala Lys Phe Ala Phe Asn Leu Tyr Arg Val Leu Lys Asp Gln
      130             135             140

Val Asn Thr Phe Asp Asn Ile Phe Ile Ala Pro Val Gly Ile Ser Thr
      145             150             155             160

Ala Met Gly Met Ile Ser Leu Gly Leu Lys Gly Glu Thr His Glu Gln
      165             170             175

Val His Ser Ile Leu His Phe Lys Asp Phe Val Asn Ala Ser Ser Lys
      180             185             190

Tyr Glu Ile Thr Thr Ile His Asn Leu Phe Arg Lys Leu Thr His Arg
      195             200             205

Leu Phe Arg Arg Asn Phe Gly Tyr Thr Leu Arg Ser Val Asn Asp Leu
      210             215             220

Tyr Ile Gln Lys Gln Phe Pro Ile Leu Leu Asp Phe Lys Thr Lys Val
      225             230             235             240

Arg Glu Tyr Tyr Phe Ala Glu Ala Gln Ile Ala Asp Phe Ser Asp Pro
      245             250             255

Ala Phe Ile Ser Lys Thr Asn Asn His Ile Met Lys Leu Thr Lys Gly
      260             265             270

Leu Ile Lys Asp Ala Leu Glu Asn Ile Asp Pro Ala Thr Gln Met Met
      275             280             285

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Ile Leu Asn Cys Ile Tyr Phe Lys Gly Ser Trp Val Asn Lys Phe Pro
290 295 300

Val Glu Met Thr His Asn His Asn Phe Arg Leu Asn Glu Arg Glu Val
305 310 315 320

Val Lys Val Ser Met Met Gln Thr Lys Gly Asn Phe Leu Ala Ser Cys
325 330 335

Leu Leu Phe Met Gly Arg Val Ala Asn Pro Ser Arg Ser
340 345

<210> 156

<211> 211

<212> PRT

<213> Homo sapiens

<400> 156

Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
1 5 10 15

Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
20 25 30

Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
35 40 45

Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
50 55 60

Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
65 70 75 80

Ala Cys Asp Asp Ala Cys Trp Arg Ile Glu Lys Val Pro Lys Val Cys
85 90 95

Arg Leu Gln Val Ser Val Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys
100 105 110

Tyr Phe Phe Asn Leu Ser Ser Met Thr Cys Glu Lys Phe Phe Ser Gly
115 120 125

Gly Cys His Arg Asn Arg Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr
130 135 140

Cys Met Gly Phe Cys Ala Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser
145 150 155 160

Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe
165 170 175

Asn Pro Arg Tyr Arg Thr Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly
180 185 190

Gly Asn Asp Asn Asn Phe Val Thr Val Gln Lys Met Arg Asp Cys Ala
195 200 205

Leu Pro Met
210

<210> 157
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 157

Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
 1 5 10 15

Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
 20 25 30

Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
 35 40 45

Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
 50 55 60

Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
 65 70 75 80

Ala Cys Asp Asp Ala Cys Trp Arg Ile Glu Lys Val Pro Lys Val Cys
 85 90 95

Arg Leu Gln Val Ser Val Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys
 100 105 110

Tyr Phe Phe Asn Leu Ser Ser Met Thr Cys Glu Lys Phe Phe Ser Gly
 115 120 125

Gly Cys His Arg Asn Arg Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr
 130 135 140

Cys Met Gly Phe Cys Ala Pro Lys Lys Lys Tyr Arg Thr Cys Asp Ala
 145 150 155 160

Phe Thr Tyr Thr Gly Cys Gly Gly Asn Asp Asn Asn Phe Val Ser Arg
 165 170 175

Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu Lys Lys Lys Lys Lys
 180 185 190

Met Pro Lys Leu Arg Phe Ala Ser Arg Ile Arg Lys Ile Arg Lys Lys
 195 200 205

Gln Phe
 210

<210> 158
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 158

Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
 1 5 10 15

Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
 20 25 30

Asp	Glu	Glu	His	Thr	Ile	Ile	Thr	Asp	Thr	Glu	Leu	Pro	Leu	Lys	
35						40				45					
Leu	Met	His	Ser	Phe	Cys	Ala	Phe	Lys	Ala	Asp	Asp	Gly	Pro	Cys	Lys
50						55				60					
Ala	Ile	Met	Lys	Arg	Phe	Phe	Phe	Asn	Ile	Phe	Thr	Arg	Gln	Cys	Glu
65				70						75				80	
Glu	Phe	Ile	Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser
				85				90						95	
Leu	Glu	Glu	Cys	Lys	Lys	Met	Cys	Thr	Arg	Asp	Asn	Ala	Asn	Arg	Ile
		100						105				110			
Ile	Lys	Thr	Thr	Leu	Gln	Gln	Glu	Lys	Pro	Asp	Phe	Cys	Phe	Leu	Glu
		115				120						125			
Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr	Phe	Tyr	Asn
130						135						140			
Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly	Cys	Leu	Gly
145				150						155				160	
Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu
				165				170						175	
Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn
		180						185				190			
Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu
195						200						205			
Phe	Gly	Lys	Asn	Leu	Val	Asp	Phe	Ile	Ala	Ser	Arg	Lys	Leu	Leu	Ser
210						215				220					
Cys															
225															

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<210> 159
<211> 636
<212> PRT
<213> Homo sapiens
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<400> 159
Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala
  1              5              10              15
Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln
          20              25              30
Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr
          35              40              45
Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
          50              55              60
Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
          65              70              75              80

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Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
 85 90 95
 Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
 100 105 110
 Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr
 115 120 125
 Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
 130 135 140
 Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met
 145 150 155 160
 Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
 165 170 175
 Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Glu Asn Thr Lys Thr Asn
 180 185 190
 Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
 195 200 205
 Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
 210 215 220
 Phe His Ser Pro Val Asp Trp Arg Leu Leu Gln Ser Lys Ser Gln Glu
 225 230 235 240
 Val Leu Ser Gln Thr Ser Thr Lys Ala Arg Lys Gln Ser Leu Phe Arg
 245 250 255
 Ala Lys Ile Lys Gly Arg Lys Glu Gly Lys Ser Arg Gln Met Glu Phe
 260 265 270
 Asn Ile Ser Lys Arg Leu Ser Cys Arg Ala Ile Val His Ser Lys Leu
 275 280 285
 Arg Gln Arg Arg Leu Gly Ala Thr Ser Leu Val Leu Gly Ser Gly Phe
 290 295 300
 Thr Phe Phe Gly Pro Tyr Leu Pro His Leu Glu Glu Glu Trp Ala Gly
 305 310 315 320
 Pro Arg Ser Thr Met Pro Tyr Ser Leu Ser Glu Gln Ile Glu Pro Lys
 325 330 335
 Lys Ala Cys Ser Leu Ser Asn Cys Ala His Gly Lys Asn Asp Val Phe
 340 345 350
 Arg Thr Tyr Cys Phe Pro Phe Leu Lys Tyr Pro Pro Asp Leu Ala Ile
 355 360 365
 Arg Asp Thr Phe Val Asn Ala Ser Arg Thr Leu Tyr Ser Ser Ser Pro
 370 375 380
 Arg Val Leu Ser Asn Asn Ser Asp Ala Asn Leu Glu Leu Ile Asn Thr
 385 390 395 400

Trp Val Ala Lys Asn Thr Asn Asn Lys Ile Ser Arg Leu Leu Asp Ser
405 410 415

Leu Pro Ser Asp Thr Arg Leu Val Leu Leu Asn Ala Ile Tyr Leu Ser
420 425 430

Ala Lys Trp Lys Thr Thr Phe Asp Pro Lys Lys Thr Arg Met Glu Pro
435 440 445

Phe His Phe Lys Asn Ser Val Ile Lys Val Pro Met Met Asn Ser Lys
450 455 460

Lys Tyr Pro Val Ala His Phe Ile Asp Gln Thr Leu Lys Ala Lys Val
465 470 475 480

Gly Gln Leu Gln Leu Ser His Asn Leu Ser Leu Val Ile Leu Val Pro
485 490 495

Gln Asn Leu Lys His Arg Leu Glu Asp Met Glu Gln Ala Leu Ser Pro
500 505 510

Ser Val Phe Lys Ala Ile Met Glu Lys Leu Glu Met Ser Lys Phe Gln
515 520 525

Pro Thr Leu Leu Thr Leu Pro Arg Ile Lys Val Thr Thr Ser Gln Asp
530 535 540

Met Leu Ser Ile Met Glu Lys Leu Glu Phe Phe Asp Phe Ser Tyr Asp
545 550 555 560

Leu Asn Leu Cys Gly Leu Thr Glu Asp Pro Asp Leu Gln Val Ser Ala
565 570 575

Met Gln His Gln Thr Val Leu Glu Leu Thr Glu Thr Gly Val Glu Ala
580 585 590

Ala Ala Ala Ser Ala Ile Ser Val Ala Arg Thr Leu Leu Val Phe Glu
595 600 605

Val Gln Gln Pro Phe Leu Phe Val Leu Trp Asp Gln Gln His Lys Phe
610 615 620

Pro Val Phe Met Gly Arg Val Tyr Asp Pro Arg Ala
625 630 635

<210> 160

<211> 389

<212> PRT

<213> Homo sapiens

<400> 160

Met Asp Val Leu Ala Glu Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu
1 5 10 15

Lys Thr Leu Gly Lys Asp Asn Ser Lys Asn Val Phe Phe Ser Pro Met
20 25 30

Ser Met Ser Cys Ala Leu Ala Met Val Tyr Met Gly Ala Lys Gly Asn
35 40 45

Thr Ala Ala Gln Met Ala Gln Ile Leu Ser Phe Asn Lys Ser Gly Gly
 50 55 60
 Gly Gly Asp Ile His Gln Gly Phe Gln Ser Leu Leu Thr Glu Val Asn
 65 70 75 80
 Lys Thr Gly Thr Gln Tyr Leu Leu Arg Met Ala Asn Arg Leu Phe Gly
 85 90 95
 Glu Lys Ser Cys Asp Phe Leu Ser Ser Phe Arg Asp Ser Cys Gln Lys
 100 105 110
 Phe Tyr Gln Ala Glu Met Glu Glu Leu Asp Phe Ile Ser Ala Val Glu
 115 120 125
 Lys Ser Arg Lys His Ile Asn Thr Trp Val Ala Glu Lys Thr Glu Gly
 130 135 140
 Lys Ile Ala Glu Leu Leu Ser Pro Gly Ser Val Asp Pro Leu Thr Arg
 145 150 155 160
 Leu Val Leu Val Asn Ala Val Tyr Phe Arg Gly Asn Trp Asp Glu Gln
 165 170 175
 Phe Asp Lys Glu Asn Thr Glu Glu Arg Leu Phe Lys Val Ser Lys Asn
 180 185 190
 Glu Glu Lys Pro Val Gln Met Met Phe Lys Gln Ser Thr Phe Lys Lys
 195 200 205
 Thr Tyr Ile Gly Glu Ile Phe Thr Gln Ile Leu Val Leu Pro Tyr Val
 210 215 220
 Gly Lys Glu Leu Asn Met Ile Ile Met Leu Pro Asp Glu Thr Thr Asp
 225 230 235 240
 Leu Arg Thr Val Glu Lys Glu Leu Thr Tyr Glu Lys Phe Val Glu Trp
 245 250 255
 Thr Arg Leu Asp Met Met Asp Glu Glu Glu Val Glu Val Ser Leu Pro
 260 265 270
 Arg Phe Lys Leu Glu Glu Ser Tyr Asp Met Glu Ser Val Leu Arg Asn
 275 280 285
 Leu Gly Met Thr Asp Ala Phe Glu Leu Gly Lys Ala Asp Phe Ser Gly
 290 295 300
 Met Ser Gln Thr Asp Leu Ser Leu Ser Lys Val Val His Lys Ser Phe
 305 310 315 320
 Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Ala Ala
 325 330 335
 Ile Met Met Met Arg Cys Ala Arg Phe Val Pro Arg Phe Cys Ala Asp
 340 345 350
 His Pro Phe Leu Phe Phe Ile Gln His Ser Cys Pro Leu Thr Leu His
 355 360 365
 Ser Val Pro Ala Thr Gln Val Ala Leu Ser Val Gln Trp Trp Gln Phe

370

375

380

Arg Asn Lys Gly Pro
385

<210> 161
<211> 204
<212> PRT
<213> Homo sapiens

<400> 161
Met Asp Val Leu Ala Glu Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu
1 5 10 15
Lys Thr Leu Gly Lys Asp Asn Ser Lys Asn Val Phe Phe Ser Pro Met
20 25 30
Ser Met Ser Cys Ala Leu Ala Met Val Tyr Met Gly Ala Lys Gly Asn
35 40 45
Thr Ala Ala Gln Met Ala Gln Ile Leu Ser Phe Asn Lys Ser Gly Gly
50 55 60
Gly Gly Asp Ile His Gln Gly Phe Gln Ser Leu Leu Thr Glu Val Asn
65 70 75 80
Lys Thr Gly Thr Gln Tyr Leu Leu Arg Met Ala Asn Arg Leu Phe Gly
85 90 95
Glu Lys Ser Cys Asp Phe Leu Ser Ser Phe Arg Asp Ser Cys Gln Lys
100 105 110
Phe Tyr Gln Ala Glu Met Glu Glu Leu Asp Phe Ile Ser Ala Val Glu
115 120 125
Lys Ser Arg Lys His Ile Asn Thr Trp Val Ala Glu Lys Thr Glu Gly
130 135 140
Lys Ile Ala Glu Leu Leu Ser Pro Gly Ser Val Asp Pro Leu Thr Arg
145 150 155 160
Leu Val Leu Val Asn Ala Val Tyr Phe Arg Gly Asn Trp Asp Glu Gln
165 170 175
Phe Asp Lys Glu Asn Thr Glu Glu Arg Leu Phe Lys Val Ser Lys Thr
180 185 190
Asn Gly Ile Leu Phe Cys Gly Arg Phe Ser Ser Pro
195 200

<210> 162
<211> 156
<212> PRT
<213> Homo sapiens

<400> 162
Met Asp Val Leu Ala Glu Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu
1 5 10 15

Lys Thr Leu Gly Lys Asp Asn Ser Lys Asn Val Phe Phe Ser Pro Met
 20 25 30
 Ser Met Ser Cys Ala Leu Ala Met Val Tyr Met Gly Ala Lys Gly Asn
 35 40 45
 Thr Ala Ala Gln Met Ala Gln Ile Leu Ser Phe Asn Lys Ser Gly Gly
 50 55 60
 Gly Gly Asp Ile His Gln Gly Phe Gln Ser Leu Leu Thr Glu Val Asn
 65 70 75 80
 Lys Thr Gly Thr Gln Tyr Leu Leu Arg Met Ala Asn Arg Leu Phe Gly
 85 90 95
 Glu Lys Ser Cys Asp Phe Leu Ser Ser Phe Arg Asp Ser Cys Gln Lys
 100 105 110
 Phe Tyr Gln Ala Glu Met Glu Glu Leu Asp Phe Ile Ser Ala Val Glu
 115 120 125
 Lys Ser Arg Lys His Ile Asn Thr Trp Val Ala Glu Lys Thr Glu Gly
 130 135 140
 Lys Met Tyr Cys Tyr Ser Thr Phe Val Ile Thr Ser
 145 150 155

<210> 163
 <211> 517
 <212> PRT
 <213> Homo sapiens

<400> 163
 Met Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly
 1 5 10 15
 Asp Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu
 20 25 30
 Pro Lys Gln Leu Pro Glu Leu Ile Arg Met Lys Arg Asp Gly Gly Arg
 35 40 45
 Leu Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly
 50 55 60
 Ser Ala Gln Gly Ala Gln Ile Gly Ala Met Leu Met Ala Ile Arg Leu
 65 70 75 80
 Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln Ala Leu Ala
 85 90 95
 Gln Ser Gly Gln Gln Leu Glu Trp Pro Glu Ala Trp Arg Gln Gln Leu
 100 105 110
 Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Lys Val Ser Leu Val
 115 120 125
 Leu Ala Pro Ala Leu Ala Ala Cys Gly Cys Lys Val Pro Met Ile Ser
 130 135 140

Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu Ser
 145 150 155 160
 Ile Pro Gly Phe Asn Val Ile Gln Ser Pro Glu Gln Met Gln Val Leu
 165 170 175
 Leu Asp Gln Ala Gly Cys Cys Ile Val Gly Gln Ser Glu Gln Leu Val
 180 185 190
 Pro Ala Asp Gly Ile Leu Tyr Ala Ala Arg Asp Val Thr Ala Thr Val
 195 200 205
 Asp Ser Leu Pro Leu Ile Thr Ala Ser Ile Leu Ser Lys Lys Leu Val
 210 215 220
 Glu Gly Leu Ser Ala Leu Val Val Asp Val Lys Phe Gly Gly Ala Ala
 225 230 235 240
 Val Phe Pro Asn Gln Glu Gln Ala Arg Glu Leu Ala Lys Thr Leu Val
 245 250 255
 Gly Val Gly Ala Ser Leu Gly Leu Arg Val Ala Ala Ala Leu Thr Ala
 260 265 270
 Met Asp Lys Pro Leu Gly Arg Cys Val Gly His Ala Leu Glu Val Glu
 275 280 285
 Glu Ala Leu Leu Cys Met Asp Gly Ala Gly Pro Pro Asp Leu Arg Asp
 290 295 300
 Leu Val Thr Thr Leu Gly Gly Ala Leu Leu Trp Leu Ser Gly His Ala
 305 310 315 320
 Gly Thr Gln Ala Gln Gly Ala Ala Arg Val Ala Ala Ala Leu Asp Asp
 325 330 335
 Gly Ser Ala Leu Gly Arg Phe Glu Arg Met Leu Ala Ala Gln Gly Val
 340 345 350
 Asp Pro Gly Leu Ala Arg Ala Leu Cys Ser Gly Ser Pro Ala Glu Arg
 355 360 365
 Arg Gln Leu Leu Pro Arg Ala Arg Glu Gln Glu Glu Leu Leu Ala Pro
 370 375 380
 Ala Asp Gly Glu Arg Ser Gly Glu Ser Pro Ser Phe Arg Leu Arg His
 385 390 395 400
 Pro Leu Pro Phe Pro Arg Pro Arg Pro Phe Pro Ser Pro Arg Leu Ser
 405 410 415
 Ala Pro Leu Pro Ala Gly Thr Val Glu Leu Val Arg Ala Leu Pro Leu
 420 425 430
 Ala Leu Val Leu His Glu Leu Gly Ala Gly Arg Ser Arg Ala Gly Glu
 435 440 445
 Pro Leu Arg Leu Gly Val Gly Ala Glu Leu Leu Val Asp Val Gly Gln
 450 455 460
 Arg Leu Arg Arg Gly Thr Pro Trp Leu Arg Val His Arg Asp Gly Pro

465 470 475 480

Ala Leu Ser Gly Pro Gln Ser Arg Ala Leu Gln Glu Ala Leu Val Leu
 485 490 495

Ser Asp Arg Ala Pro Phe Ala Ala Pro Ser Pro Phe Ala Glu Leu Val
 500 505 510

Leu Pro Pro Gln Gln
 515

<210> 164
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 164

Met Ser Asp Ala Ser Leu Arg Ser Thr Ser Thr Met Glu Arg Leu Val
 1 5 10 15

Ala Arg Gly Thr Phe Pro Val Leu Val Arg Thr Ser Ala Cys Arg Ser
 20 25 30

Leu Phe Gly Pro Val Asp His Glu Glu Leu Ser Arg Glu Leu Gln Ala
 35 40 45

Arg Leu Ala Glu Leu Asn Ala Glu Asp Gln Asn Arg Trp Asp Tyr Asp
 50 55 60

Phe Gln Gln Asp Met Pro Leu Arg Gly Pro Gly Arg Leu Gln Trp Thr
 65 70 75 80

Glu Val Asp Ser Asp Ser Val Pro Ala Phe Tyr Arg Glu Thr Val Gln
 85 90 95

Ile Ser Ser Pro Ser Ala Arg Asp Gln Arg Leu Arg Ser Arg Arg Ala
 100 105 110

Met Ser Pro Arg Arg Val Pro Leu Gln Ala Pro Pro Leu Ala Trp Ala
 115 120 125

Arg Trp Ser Arg Pro Arg Ala Arg Gly Cys Gly Glu Pro Ile
 130 135 140

<210> 165
 <211> 561
 <212> PRT
 <213> Homo sapiens

<400> 165

Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala Ile
 1 5 10 15

Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
 20 25 30

Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
 35 40 45

Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
 50 55 60
 Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
 65 70 75 80
 Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
 85 90 95
 Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
 100 105 110
 Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
 115 120 125
 Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
 130 135 140
 Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
 145 150 155 160
 Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
 165 170 175
 Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
 180 185 190
 Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
 195 200 205
 Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
 210 215 220
 Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
 225 230 235 240
 Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
 245 250 255
 Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
 260 265 270
 Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
 275 280 285
 Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
 290 295 300
 Tyr Val Thr Val Leu Lys Thr Ala Gly Ala Asn Thr Thr Asp Lys Glu
 305 310 315 320
 Leu Glu Val Leu Ser Leu His Asn Val Thr Phe Glu Asp Ala Gly Glu
 325 330 335
 Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Phe Ser His His Ser Ala
 340 345 350
 Trp Leu Val Val Leu Pro Ala Glu Glu Glu Leu Val Glu Ala Asp Glu
 355 360 365
 Ala Gly Ser Val Tyr Ala Gly Ile Leu Ser Tyr Gly Val Gly Phe Phe

370 375 380
 Leu Phe Ile Leu Val Val Ala Ala Val Thr Xaa Cys Arg Leu Arg Ser
 385 390 395 400
 Pro Pro Lys Lys Gly Leu Gly Ser Pro Thr Val His Lys Ile Ser Arg
 405 410 415
 Phe Pro Leu Lys Arg Gln Val Ser Leu Glu Ser Asn Ala Ser Met Ser
 420 425 430
 Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly Glu Gly
 435 440 445
 Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp Pro Lys
 450 455 460
 Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu Gly Glu
 465 470 475 480
 Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile Asp Lys
 485 490 495
 Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu Lys Asp
 500 505 510
 Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
 515 520 525
 Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gln Val
 530 535 540
 Pro Met Leu Leu Asp Val Thr Ser Leu Tyr Ile Ser Ile Tyr Ile Ile
 545 550 555 560
 Tyr

<210> 166
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 166
 Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
 1 5 10 15
 Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
 20 25 30
 Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
 35 40 45
 Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
 50 55 60
 Leu Tyr Gly Gly Cys Glu Gly Asn Arg Asn Asn Phe Tyr Thr Trp Glu
 65 70 75 80
 Ala Cys Asp Asp Ala Cys Trp Arg Ile Glu Lys Val Pro Lys Val Cys

85 90 95
 Arg Leu Gln Val Ser Val Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys
 100 105 110
 Tyr Phe Phe Asn Leu Ser Ser Met Thr Cys Glu Lys Phe Phe Ser Gly
 115 120 125
 Gly Cys His Arg Asn Arg Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr
 130 135 140
 Cys Met Gly Phe Cys Ala Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser
 145 150 155 160
 Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe
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 Asn Ile Asp Val Ser Ile Ser Thr Ala Val Lys Leu
 180 185

<210> 167
 <211> 539
 <212> PRT
 <213> Homo sapiens

<400> 167
 Met Asn Gln Leu Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg
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 Ser Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro
 20 25 30
 Glu Pro Arg Lys Pro Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly
 35 40 45
 Ser Cys Ala Pro Cys Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln
 50 55 60
 Leu Cys Pro Gly Cys Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr
 65 70 75 80
 Ser Gly Ala Phe Lys Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe
 85 90 95
 Val Lys His Ser Thr Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg
 100 105 110
 Asp Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp
 115 120 125
 Glu Tyr Lys Asp Cys His Leu Ala Gln Val Pro Ser His Thr Val Val
 130 135 140
 Ala Arg Ser Met Gly Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn
 145 150 155 160
 Gln Ala Gln Glu His Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu
 165 170 175
 Phe Ser Ser Pro His Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His

180										185					190					
Gly	Phe	Leu	Lys	Val	Pro	Pro	Arg	Met	Asp	Ala	Lys	Met	Tyr	Leu	Gly					
		195					200					205								
Tyr	Glu	Tyr	Val	Thr	Ala	Ile	Arg	Asn	Leu	Arg	Glu	Gly	Thr	Cys	Pro					
	210					215					220									
Glu	Ala	Pro	Thr	Asp	Glu	Cys	Lys	Pro	Val	Lys	Trp	Cys	Ala	Leu	Ser					
225					230					235					240					
His	His	Glu	Arg	Leu	Lys	Cys	Asp	Glu	Trp	Ser	Val	Asn	Ser	Val	Gly					
				245					250					255						
Lys	Ile	Glu	Cys	Val	Ser	Ala	Glu	Thr	Thr	Glu	Asp	Cys	Ile	Ala	Lys					
			260					265					270							
Ile	Met	Asn	Gly	Glu	Ala	Asp	Ala	Met	Ser	Leu	Asp	Gly	Gly	Phe	Val					
		275					280					285								
Tyr	Ile	Ala	Gly	Lys	Cys	Gly	Leu	Val	Pro	Val	Leu	Ala	Glu	Asn	Tyr					
	290					295					300									
Asn	Lys	Ser	Asp	Asn	Cys	Glu	Asp	Thr	Pro	Glu	Ala	Gly	Tyr	Phe	Ala					
305					310					315					320					
Val	Ala	Val	Val	Lys	Lys	Ser	Ala	Ser	Asp	Leu	Thr	Trp	Asp	Asn	Leu					
				325					330					335						
Lys	Gly	Lys	Lys	Ser	Cys	His	Thr	Ala	Val	Gly	Arg	Thr	Ala	Gly	Trp					
			340					345					350							
Asn	Ile	Pro	Met	Gly	Leu	Leu	Tyr	Asn	Lys	Ile	Asn	His	Cys	Glu	Pro					
		355					360					365								
Asn	Asn	Lys	Glu	Gly	Tyr	Tyr	Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu					
	370					375					380									
Val	Glu	Lys	Gly	Asp	Val	Ala	Phe	Val	Lys	His	Gln	Thr	Val	Pro	Gln					
385					390					395					400					
Asn	Thr	Gly	Gly	Lys	Asn	Pro	Asp	Pro	Trp	Ala	Lys	Asn	Leu	Asn	Glu					
				405					410					415						
Lys	Asp	Tyr	Glu	Leu	Leu	Cys	Leu	Asp	Gly	Thr	Arg	Lys	Pro	Val	Glu					
			420					425					430							
Glu	Tyr	Ala	Asn	Cys	His	Leu	Ala	Arg	Ala	Pro	Asn	His	Ala	Val	Val					
		435					440					445								
Thr	Arg	Lys	Asp	Lys	Glu	Ala	Cys	Val	His	Lys	Ile	Leu	Arg	Gln	Gln					
	450					455					460									
Gln	His	Leu	Phe	Gly																

Glu Glu Tyr Val Lys Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser
 515 520 525

Ser Leu Leu Glu Ala Cys Thr Phe Arg Arg Pro
 530 535

<210> 168
 <211> 77
 <212> PRT
 <213> Homo sapiens

<400> 168
 Met Arg Thr Leu Leu Pro Pro Ala Leu Leu Thr Cys Trp Leu Leu Ala
 1 5 10 15

Pro Val Asn Ser Ile His Pro Glu Cys Arg Phe His Leu Glu Ile Gln
 20 25 30

Glu Glu Glu Thr Lys Cys Ala Glu Leu Leu Arg Ser Gln Thr Glu Lys
 35 40 45

His Lys Gly His Thr Lys Gly Phe Ile Leu Ile His Ala Gly Gly Leu
 50 55 60

Lys Arg Ile Leu Asp Pro His Thr Tyr Pro Leu Ala Pro
 65 70 75

<210> 169
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 169
 Met Lys Leu Pro Glu Val Cys Phe Phe Asn Cys Cys Thr Leu His Glu
 1 5 10 15

Ser Lys Tyr Glu Ile Val Thr Met Phe Ile Tyr Phe Asn Trp Leu Tyr
 20 25 30

Phe Phe Pro Ala Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu
 35 40 45

Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser
 50 55 60

Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg
 65 70 75 80

Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile
 85 90 95

Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn
 100 105 110

Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe
 115 120 125

Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg

130		135		140
Lys Lys Gln Arg Val	Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn			
145	150	155		160

Met

<210> 170
 <211> 157
 <212> PRT
 <213> Mouse

<400> 170
 Met Tyr Asn Thr Ser Xaa Met Xaa Pro Xaa Asn Pro Arg Pro Ile Leu
 1 5 10 15

Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asp
 20 25 30

Ser Phe Glu Val Arg Val Cys Ala Ser Pro Gly Arg Asp Pro Arg Thr
 35 40 45

Glu Glu Glu Asn Phe Arg Lys Lys Glu Val Leu Cys Pro Glu Leu Pro
 50 55 60

Pro Gly Ser Ala Lys Arg Ala Leu Pro Thr Cys Thr Ser Ala Ser Pro
 65 70 75 80

Pro Gln Lys Lys Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Lys Ile
 85 90 95

Arg Gly Arg Lys Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu
 100 105 110

Glu Leu Lys Asp Ala His Ala Thr Glu Glu Ser Gly Asp Ser Arg Ala
 115 120 125

His Ser Ser Tyr Leu Lys Thr Lys Lys Gly Gln Ser Thr Ser Arg His
 130 135 140

Lys Lys Thr Met Val Lys Lys Val Gly Pro Asp Ser Asp
 145 150 155

<210> 171
 <211> 157
 <212> PRT
 <213> Mouse

<400> 171
 Met Phe Asn Arg Ser Cys Leu Arg Gly Met Asn Pro Arg Pro Ile Leu
 1 5 10 15

Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asp
 20 25 30

Ser Phe Glu Val Arg Val Cys Ala Ser Pro Gly Arg Asp Pro Arg Thr
 35 40 45

Glu Glu Glu Asn Phe Arg Lys Lys Glu Val Leu Cys Pro Glu Leu Pro
 50 55 60

Pro Gly Ser Ala Lys Arg Ala Leu Pro Thr Cys Thr Ser Ala Ser Pro
 65 70 75 80

Pro Gln Lys Lys Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Lys Ile
 85 90 95

Arg Gly Arg Lys Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu
 100 105 110

Glu Leu Lys Asp Ala His Ala Thr Glu Glu Ser Gly Asp Ser Arg Ala
 115 120 125

His Ser Ser Tyr Leu Lys Thr Lys Lys Gly Gln Ser Thr Ser Arg His
 130 135 140

Lys Lys Thr Met Val Lys Lys Val Gly Pro Asp Ser Asp
 145 150 155

<210> 172

<211> 1252

<212> PRT

<213> Mouse

<400> 172

Met Gly Ala Ala Ser Gly Gln Arg Gly Arg Trp Pro Leu Ser Pro Pro
 1 5 10 15

Leu Leu Met Leu Ser Leu Leu Val Leu Leu Leu Gln Pro Ser Pro Ala
 20 25 30

Pro Ala Leu Asp Pro Gly Leu Gln Pro Gly Asn Phe Ser Pro Asp Glu
 35 40 45

Ala Gly Ala Gln Leu Phe Ala Glu Ser Tyr Asn Ser Ser Ala Glu Val
 50 55 60

Val Met Phe Gln Ser Thr Val Ala Ser Trp Ala His Asp Thr Asn Ile
 65 70 75 80

Thr Glu Glu Asn Ala Arg Arg Gln Glu Glu Ala Ala Leu Val Ser Gln
 85 90 95

Glu Phe Ala Glu Val Trp Gly Lys Lys Ala Lys Glu Leu Tyr Glu Ser
 100 105 110

Ile Trp Gln Asn Phe Thr Asp Ser Lys Leu Arg Arg Ile Ile Gly Ser
 115 120 125

Ile Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Gln Arg Gln Gln
 130 135 140

Tyr Asn Ser Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr Gly Lys
 145 150 155 160

Val Cys Phe Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Glu
 165 170 175

Leu Thr Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Lys Leu Leu Phe
 180 185 190
 Ala Trp Glu Gly Trp His Asp Ala Val Gly Ile Pro Leu Lys Pro Leu
 195 200 205
 Tyr Gln Asp Phe Thr Ala Ile Ser Asn Glu Ala Tyr Arg Gln Asp Asp
 210 215 220
 Phe Ser Asp Thr Gly Ala Phe Trp Arg Ser Trp Tyr Glu Ser Pro Ser
 225 230 235 240
 Phe Glu Glu Ser Leu Glu His Ile Tyr His Gln Leu Glu Pro Leu Tyr
 245 250 255
 Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg Arg Tyr Gly
 260 265 270
 Asp Lys Tyr Val Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly
 275 280 285
 Asp Met Trp Ala Gln Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro
 290 295 300
 Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln Lys
 305 310 315 320
 Gly Trp Asn Ala Thr His Met Phe Arg Val Ser Glu Glu Phe Phe Thr
 325 330 335
 Ser Leu Gly Leu Ser Pro Met Pro Pro Glu Phe Trp Ala Glu Ser Met
 340 345 350
 Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser Ala
 355 360 365
 Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg
 370 375 380
 Val Thr Met Glu Gln Leu Ala Thr Val His His Glu Met Gly His Val
 385 390 395 400
 Gln Tyr Tyr Leu Gln Tyr Lys Asp Leu His Val Ser Leu Arg Arg Gly
 405 410 415
 Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser
 420 425 430
 Val Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp His Val
 435 440 445
 Thr Asn Asp Ile Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu
 450 455 460
 Glu Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg
 465 470 475 480
 Trp Gly Val Phe Ser Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp
 485 490 495
 Trp Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Ala

500					505					510						
Arg	Asn	Glu	Thr	His	Phe	Asp	Ala	Gly	Ala	Lys	Phe	His	Ile	Pro	Asn	
515					520					525						
Val	Thr	Pro	Tyr	Ile	Arg	Tyr	Phe	Val	Ser	Phe	Val	Leu	Gln	Phe	Gln	
530					535					540						
Phe	His	Gln	Ala	Leu	Cys	Lys	Glu	Ala	Gly	His	Gln	Gly	Pro	Leu	His	
545					550					555					560	
Gln	Cys	Asp	Ile	Tyr	Gln	Ser	Ala	Gln	Ala	Gly	Ala	Lys	Leu	Lys	Gln	
565					570					575						
Val	Leu	Gln	Ala	Gly	Cys	Ser	Arg	Pro	Trp	Gln	Glu	Val	Leu	Lys	Asp	
580					585					590						
Leu	Val	Gly	Ser	Asp	Ala	Leu	Asp	Ala	Lys	Ala	Leu	Leu	Glu	Tyr	Phe	
595					600					605						
Gln	Pro	Val	Ser	Gln	Trp	Leu	Glu	Glu	Gln	Asn	Gln	Arg	Asn	Gly	Glu	
610					615					620						
Val	Leu	Gly	Trp	Pro	Glu	Asn	Gln	Trp	Arg	Pro	Pro	Leu	Pro	Asp	Asn	
625					630					635					640	
Tyr	Pro	Glu	Gly	Ile	Asp	Leu	Glu	Thr	Asp	Glu	Ala	Lys	Ala	Asp	Arg	
645					650					655						
Phe	Val	Glu	Glu	Tyr	Asp	Arg	Thr	Ala	Gln	Val	Leu	Leu	Asn	Glu	Tyr	
660					665					670						
Ala	Glu	Ala	Asn	Trp	Gln	Tyr	Asn	Thr	Asn	Ile	Thr	Ile	Glu	Gly	Ser	
675					680					685						
Lys	Ile	Leu	Leu	Glu	Lys	Ser	Thr	Glu	Val	Ser	Asn	His	Thr	Leu	Lys	
690					695					700						
Tyr	Gly	Thr	Arg	Ala	Lys	Thr	Phe	Asp	Val	Ser	Asn	Phe	Gln	Asn	Ser	
705					710					715					720	
Ser	Ile	Lys	Arg	Ile	Ile	Lys	Lys	Leu	Gln	Asn	Leu	Asp	Arg	Ala	Val	
725					730					735						
Leu	Pro	Pro	Lys	Glu	Leu	Glu	Glu	Tyr	Asn	Gln	Ile	Leu	Leu	Asp	Met	
740					745					750						
Glu	Thr	Thr	Tyr	Ser	Leu	Ser	Asn	Ile	Cys	Tyr	Thr	Asn	Gly	Thr	Cys	
755					760					765						
Met	Pro	Leu	Glu	Pro	Asp	Leu	Thr	Asn	Met	Met	Ala	Thr	Ser	Arg	Lys	
770					775					780						
Tyr	Glu	Glu	Leu	Leu	Trp	Ala	Trp	Lys	Ser	Trp	Arg	Asp	Lys	Val	Gly	
785					790					795					800	
Arg	Ala	Ile	Leu	Pro	Phe	Phe	Pro	Lys	Tyr	Val	Glu	Phe	Ser	Asn	Lys	
805					810					815						
Ile	Ala	Lys	Leu	Asn	Gly	Tyr	Thr	Asp	Ala	Gly	Asp	Ser	Trp	Arg	Ser	
820					825					830						

Leu Tyr Glu Ser Asp Asn Leu Glu Gln Asp Leu Glu Lys Leu Tyr Gln
 835 840 845
 Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ser
 850 855 860
 Leu His Arg His Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly Pro Ile
 865 870 875 880
 Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile
 885 890 895
 Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Pro Asn Ile Asp Ala Thr
 900 905 910
 Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys Glu
 915 920 925
 Ala Asp Asn Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu
 930 935 940
 Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val
 945 950 955 960
 Val Cys His Pro Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg
 965 970 975
 Ile Lys Gln Cys Thr Ser Val Asn Met Glu Asp Leu Val Ile Ala His
 980 985 990
 His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro
 995 1000 1005
 Val Thr Phe Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly
 1010 1015 1020
 Asp Ile Met Ala Leu Ser Val Ser Thr Pro Lys His Leu Tyr Ser Leu
 1025 1030 1035 1040
 Asn Leu Leu Ser Thr Glu Gly Ser Gly Tyr Glu Tyr Asp Ile Asn Phe
 1045 1050 1055
 Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr
 1060 1065 1070
 Leu Ile Asp Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys
 1075 1080 1085
 Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly
 1090 1095 1100
 Leu Cys Pro Pro Val Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ser
 1105 1110 1115 1120
 Lys Phe His Val Pro Ala Asn Val Pro Tyr Val Arg Tyr Phe Val Ser
 1125 1130 1135
 Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Arg Ala Ala Gly
 1140 1145 1150

His Thr Gly Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala
 1155 1160 1165

Gly Lys Leu Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp
 1170 1175 1180

Pro Glu Ala Met Lys Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser
 1185 1190 1195 1200

Ala Met Met Asn Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr Glu
 1205 1210 1215

Asn Arg Arg His Gly Glu Thr Leu Gly Trp Pro Glu Tyr Asn Trp Ala
 1220 1225 1230

Pro Asn Thr Gly Thr Thr Pro Thr Leu Pro Pro Ala Pro Ile Leu Trp
 1235 1240 1245

Ile Pro Ser Val
 1250

<210> 173
 <211> 374
 <212> PRT
 <213> Mouse

<400> 173

Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His
 1 5 10 15

Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys
 20 25 30

Met Pro Met Glu Arg Ala Leu Gly Glu Val Tyr Val Asp Asn Ser Lys
 35 40 45

Pro Thr Val Phe Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
 50 55 60

Ala Ala Ala Ala Ala Ala Ala Ala Ser Ala Pro Val Tyr Gly Gln Ser
 65 70 75 80

Gly Ile Ala Tyr Gly Pro Gly Ser Glu Ala Ala Ala Phe Ser Ala Asn
 85 90 95

Ser Leu Gly Ala Phe Pro Gln Leu Asn Ser Val Ser Pro Ser Pro Leu
 100 105 110

Met Leu Leu His Pro Pro Pro Gln Leu Ser Pro Phe Leu His Pro His
 115 120 125

Gly Gln Gln Val Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Ala Tyr Ala
 130 135 140

Val Arg Asp Thr Gly Pro Pro Ala Phe Tyr Arg Ser Asn Ser Asp Asn
 145 150 155 160

Arg Arg Gln Asn Gly Arg Glu Arg Leu Ser Ser Ser Asn Glu Lys Gly
 165 170 175

Asn Met Ile Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys
 180 185 190

Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly
 195 200 205

Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met
 210 215 220

Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser
 225 230 235 240

Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys
 245 250 255

Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys
 260 265 270

Arg Gln Arg Asp Asp Leu Glu Gly Arg Asn Glu Met Gly Ala Ser Gly
 275 280 285

Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Val Ile Lys His
 290 295 300

Thr Lys Lys Asn Ser Pro Ala Leu Ser Leu Thr Ala Asp Gln Met Val
 305 310 315 320

Ser Ala Leu Leu Asp Ala Glu Pro Pro Met Ile Tyr Ser Glu Tyr Asp
 325 330 335

Pro Ser Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn
 340 345 350

Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val
 355 360 365

Pro Gly Gly Asn Ser Leu
 370

<210> 174
 <211> 468
 <212> PRT
 <213> Mouse

<400> 174
 Met Ala Thr Leu Leu Arg Ser Lys Leu Thr Asn Val Ala Thr Ser Val
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Ser Asn Lys Ser Gln Ala Lys Val Ser Gly Met Phe Ala Arg Met Gly
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Phe Gln Ala Ala Thr Asp Glu Glu Ala Val Gly Phe Ala His Cys Asp
 35 40 45

Asp Leu Asp Phe Glu His Arg Gln Gly Leu Gln Met Asp Ile Leu Lys
 50 55 60

Ser Glu Gly Glu Pro Cys Gly Asp Glu Gly Ala Glu Ala Pro Val Glu
 65 70 75 80

Gly	Asp	Ile	His	Tyr	Gln	Arg	Gly	Gly	Ala	Pro	Leu	Pro		Ser	Gly	
				85					90					95		
Ser	Lys	Asp	Gln	Ala	Val	Gly	Ala	Gly	Gly	Glu	Phe	Gly	Gly	His	Asp	
				100					105					110		
Lys	Pro	Lys	Ile	Thr	Ala	Trp	Glu	Ala	Gly	Trp	Asn	Val	Thr	Asn	Ala	
				115					120					125		
Ile	Gln	Gly	Met	Phe	Val	Leu	Gly	Leu	Pro	Tyr	Ala	Ile	Leu	His	Gly	
				130					135					140		
Gly	Tyr	Leu	Gly	Leu	Phe	Leu	Ile	Ile	Phe	Ala	Ala	Val	Val	Cys	Cys	
				145					150					155		
Tyr	Thr	Gly	Lys	Ile	Leu	Ile	Ala	Cys	Leu	Tyr	Glu	Glu	Asn	Glu	Asp	
				165					170					175		
Gly	Glu	Val	Val	Arg	Val	Arg	Asp	Ser	Tyr	Val	Ala	Ile	Ala	Asn	Ala	
				180					185					190		
Cys	Cys	Ala	Pro	Arg	Phe	Pro	Thr	Leu	Gly	Gly	Arg	Val	Val	Asn	Val	
				195					200					205		
Ala	Gln	Ile	Ile	Glu	Leu	Val	Met	Thr	Cys	Ile	Leu	Tyr	Val	Val	Val	
				210					215					220		
Ser	Gly	Asn	Leu	Met	Tyr	Asn	Ser	Phe	Pro	Gly	Leu	Pro	Val	Ser	Gln	
				225					230					235		
Lys	Ser	Trp	Ser	Ile	Ile	Ala	Thr	Ala	Val	Leu	Leu	Pro	Cys	Ala	Phe	
				245					250					255		
Leu	Lys	Asn	Leu	Lys	Ala	Val	Ser	Lys	Phe	Ser	Leu	Leu	Cys	Thr	Leu	
				260					265					270		
Ala	His	Phe	Val	Ile	Asn	Ile	Leu	Val	Ile	Ala	Tyr	Cys	Leu	Ser	Arg	
				275					280					285		
Ala	Arg	Asp	Trp	Ala	Trp	Glu	Lys	Val	Lys	Phe	Tyr	Ile	Asp	Val	Lys	
				290					295					300		
Lys	Phe	Pro	Ile	Ser	Ile	Gly	Ile	Ile	Val	Phe	Ser	Tyr	Thr	Ser	Gln	
				305					310					315		
Ile	Phe	Leu	Pro	Ser	Leu	Glu	Gly	Asn	Met	Gln	Gln	Pro	Ser	Glu	Phe	
				325					330					335		
His	Cys	Met	Met	Asn	Trp	Thr	His	Ile	Ala	Ala	Cys	Val	Leu	Lys	Gly	
				340					345					350		
Leu	Phe	Ala	Leu	Val	Ala	Tyr	Leu	Thr	Trp	Ala	Asp	Glu	Thr	Lys	Glu	
				355					360					365		
Val	Ile	Thr	Asp	Asn	Leu	Pro	Gly	Ser	Ile	Arg	Ala	Val	Val	Asn	Leu	
				370					375					380		
Phe	Leu	Val	Ala	Lys	Ala	Leu	Leu	Ser	Tyr	Pro	Leu	Pro	Phe	Phe	Ala	
				385					390					395		
Ala	Val	Glu	Val	Leu	Glu	Lys	Ser	Leu	Phe	Gln	Glu	Gly	Ser	Arg	Ala	

405										410					415				
Phe	Phe	Pro	Ala	Cys	Tyr	Gly	Gly	Asp	Gly	Arg	Leu	Lys	Ser	Trp	Gly				
			420					425					430						
Leu	Thr	Leu	Arg	Cys	Ala	Leu	Val	Val	Phe	Thr	Leu	Leu	Met	Ala	Ile				
			435					440					445						
Ser	Ser	Cys	Ala	Met	Tyr	Pro	Phe	Val	Glu	Leu	Tyr	Thr	Val	Arg	Val				
			450					455					460						
Val	Cys	Ser	Trp																
465																			

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- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW). Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM). European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR). OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:
— with international search report
- (88) Date of publication of the international search report:
3 January 2002
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 01/36632 A3

(54) Title: VARIANTS OF ALTERNATIVE SPLICING

(57) Abstract: The present invention concerns novel variants, amino acid and nucleic acid sequences obtained by alternative splicing of known sequences, expression vectors and host cells containing the variants' nucleic acid sequence, and antibodies reactive with the variants' products. The invention also concerns pharmaceutical compositions containing any of the above as well as methods of detection. A preferred example is the angiotensin converting enzyme (ACE) variant.

International Application No.

PCT/IL 00/00766

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/57 C07K14/47 C07K14/705 C12N9/48
 C12Q1/68 G01N33/68 G01N33/50 A61K38/17 A61K38/48

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N A61K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EMBASE, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GB 2 264 948 A (MERCK & CO INC) 15 September 1993 (1993-09-15) figure 3 page 41 -page 42, line 7	2,8,9, 20-22
A	claims 9-14	1-30
X	WO 93 25677 A (GARVAN INST MED RES ;PIERCE KERRIE DIANE (AU); SELBIE LISA (AU); F) 23 December 1993 (1993-12-23)	2,8,9, 20-22
A	the whole document	1-30
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

30 July 2001

Date of mailing of the international search report

13.08.01

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Andres, S

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IL 00/00766

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	FURLONG T J ET AL: "MOLECULAR CHARACTERIZATION OF A HUMAN BRAIN ADENOSINE A2 RECEPTOR" MOLECULAR BRAIN RESEARCH, vol. 15, no. 1/02, 1 September 1992 (1992-09-01), pages 62-66, XP000615546 ISSN: 0169-328X the whole document	2,8,9
X	----- DATABASE EM_HUM 'Online! EMBL; Accession number : U40771; ID : HS2AAR02, 15 December 1995 (1995-12-15) "Human A2a adenosine receptor subtype (ADORA2A) gene" XP002165717 abstract	2
A	----- GELFAND M S ET AL: "ASDB: Database of alternatively spliced genes." NUCLEIC ACIDS RESEARCH, vol. 27, no. 1, 1 January 1999 (1999-01-01), pages 301-302, XP002165716 ISSN: 0305-1048 cited in the application	
A	----- CHU Y Y ET AL: "Characterization of the rat A2a adenosine receptor gene." DNA AND CELL BIOLOGY, (1996 APR) 15 (4) 329-37., XP000992998	
X	----- BERNSTEIN K E ET AL: "THE ISOLATION OF ANGIOTENSIN-CONVERTING ENZYME CDNA" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 263, no. 23, 15 August 1988 (1988-08-15), pages 11021-11024, XP000095152 ISSN: 0021-9258	2,8,9, 32,38,39
Y	the whole document	1-22, 25-53, 56-61
Y	----- SUGIMURA K ET AL.: "Alternative splicing of the mRNA coding for the human endothelial angiotensin-converting enzyme: a new mechanism for solubilization." BIOCHEM BIOPHYS RES COMMUN 1998 JUN 18;247(2):466-72., XP002173427 the whole document	1-22, 25-53, 56-61

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	BERNSTEIN K E ET AL: "MOUSE ANGIOTENSIN-CONVERTING ENZYME IS A PROTEIN COMPOSED OF TWO HOMOLOGOUS DOMAINS" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 264, no. 20, 1989, pages 11945-11951, XP002173428 ISSN: 0021-9258 the whole document ---	2,8,9, 32,38,39
X	WO 90 03435 A (INST NAT SANTE RECH MED) 5 April 1990 (1990-04-05) the whole document ---	2,8-13, 32,38-44
X	WO 85 00369 A (CHIRON CORP) 31 January 1985 (1985-01-31) the whole document ---	2,8,9
X	DATABASE EM_EST 'Online! EMBL; Accession number : AI790464, 4 July 1999 (1999-07-04) MARRA, M. ET AL.: "u101e02.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2064794 3' " XP002173429 abstract ---	2
Y	WHITE R ET AL: "STRUCTURAL ORGANIZATION AND EXPRESSION OF THE MOUSE ESTROGEN RECEPTOR" MOLECULAR ENDOCRINOLOGY, vol. 1, no. 10, 1987, pages 735-744, XP001002989 ISSN: 0888-8809 the whole document ---	1-22, 25-30
Y	LU B ET AL: "Estrogen receptor-beta mRNA variants in human and murine tissues." MOLECULAR AND CELLULAR ENDOCRINOLOGY, vol. 138, no. 1-2, 16 March 1998 (1998-03-16), pages 199-203, XP001002992 ISSN: 0303-7207 the whole document ---	1-22, 25-30
X	KOIKE S ET AL: "MOLECULAR CLONING AND CHARACTERIZATION OF RAT ESTROGEN RECEPTOR CDNA" NUCLEIC ACIDS RESEARCH, vol. 15, no. 6, 25 March 1987 (1987-03-25), pages 2499-2513, XP002026307 ISSN: 0305-1048 the whole document ---	2,8,9

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/IL 00/00766

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	PFEFFER ULRICH ET AL: "Alternative splicing of the estrogen receptor primary transcript normally occurs in estrogen receptor positive tissues and cell lines." JOURNAL OF STEROID BIOCHEMISTRY AND MOLECULAR BIOLOGY, vol. 56, no. 1-6, 1996, pages 99-105, XP001002991 ISSN: 0960-0760 the whole document	1-22, 25-30
T	WO 01 00823 A (EUROP MOLECULAR BIOLOGY LAB ;DENGIER STEFANIE (IT); FLOURIOT GILLES) 4 January 2001 (2001-01-04)	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IL 00/00766

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 23 24 54 55
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-61 (inventions 1, 30 and 31)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 23 24 54 55

Present claims 23, 24, 54 and 55 relate to compounds defined by reference to a desirable characteristic or property, namely their capacity to be an activator or deactivator of a particular protein.

The claims cover all compounds having this characteristic or property, whereas the application provides no support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for any of such compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search impossible. Consequently, no search has been carried out for these claims.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Invention 1: Claims 1-30 (all partially)

A nucleic acid sequence defined by SEQ ID 1 and its corresponding aminoacid sequence SEQ ID 88. An antibody binding specifically to the protein, vectors and hosts expressing the nucleic acid, pharmaceutical compositions containing them and their uses in therapy or diagnostic.

2. Claims: Invention 2: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 2 and 89.

3. Claims: Invention 3: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 3 and 90.

4. Claims: Invention 4: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 4,5,91 and 92.

5. Claims: Invention 5: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 6 and 93.

6. Claims: Invention 6: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 7 and 94.

7. Claims: Invention 7: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 8 and 95.

8. Claims: Invention 8: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 9,10,96 and 97.

9. Claims: Invention 9: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 11 and 98.

10. Claims: Invention 10: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 12 and 99.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

11. Claims: Invention 11: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 13-16 and 100-103.
12. Claims: Invention 12: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 17-19,104-106 and 163.
13. Claims: Invention 13: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 20,107 and 159.
14. Claims: Invention 14: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 21-24,61,62, 108-111,149,150 and 160-162.
15. Claims: Invention 15: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 25 and 112.
16. Claims: Invention 16: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 26,27,113 and 114.
17. Claims: Invention 17: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 28,64,115,152 and 164.
18. Claims: Invention 18: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 29,116 and 139.
19. Claims: Invention 19: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 30-34,52-55,117-121 and 140-143.
20. Claims: Invention 20: Claims 1-30 (all partially)
As for subject 1, but concerning SEQ IDs 35,122,170 and 171.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

21. Claims: Invention 21: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 36 and 123.

22. Claims: Invention 22: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 37,38,124,125 and 167.

23. Claims: Invention 23: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 39 and 126.

24. Claims: Invention 24: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 40,45,46,127, 132,133 and 168.

25. Claims: Invention 25: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 41 and 128.

26. Claims: Invention 26: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 42,43,48-50, 129,130 and 135-137.

27. Claims: Invention 27: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 44 and 131.

28. Claims: Invention 28: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 47 and 134.

29. Claims: Invention 29: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 51,138 and 165.

30. Claims: Invention 30: Claims 1-30 (all partially) and
claims 31-61

As for subject 1, but concerning SEQ IDs 56,85,144 and 172.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

31. Claims: Invention 31: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 57,145 and 173.

32. Claims: Invention 32: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 58 and 146.

33. Claims: Invention 33: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 59 and 147.

34. Claims: Invention 34: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 60,148 and 174.

35. Claims: Invention 35: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 63 and 151.

36. Claims: Invention 36: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 65 and 153.

37. Claims: Invention 37: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 66 and 154.

38. Claims: Invention 38: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 67 and 155.

39. Claims: Invention 39: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 68,69,156,157 and 166.

40. Claims: Invention 40: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 70,158 and 169.

41. Claims: Inventions 41 to 56: Claims 1-30 (all partially)

As for subject 1, but concerning SEQ IDs 71-84, 86 and 87

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

respectively.

INTERNATIONAL SEARCH REPORT

Information on patent family members

In International Application No

PCT/IL 00/00766

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
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			EP 0644935 A	29-03-1995
			JP 8500967 T	06-02-1996
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